GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:　　December 21, 2005, 14:17:53 ; Search time 152.239 Seconds
　　　　　　　　　　　　　　　　　　　　　(without alignments)
　　　　　　　　　　　　　　　　　　　1313.181 Million cell updates/sec

Title:
Perfect score:　2450
Sequence:　　　1 MGPPHSGPGGVRVGALLLLG............TTLLRQRASVEAEAGQHGPL 455

Scoring table:　US-10-021-121-2
　　　　　　　　BLOSUM62
　　　　　　　　Gapop 10.0 , Gapext 0.5

Searched:　2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters:　　2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
　　　　　　　　　Maximum Match 100%
　　　　　　　　　Listing first 45 summaries

Database :　A_Geneseq_21:*
　　　　　　1: geneseqp1980s:*
　　　　　　2: geneseqp1990s:*
　　　　　　3: geneseqp2000s:*
　　　　　　4: geneseqp2001s:*
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　　　　　　6: geneseqp2003as:*
　　　　　　7: geneseqp2003bs:*
　　　　　　8: geneseqp2004s:*
　　　　　　9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2450	100.0	455	2	AAW33698	Aaw33698 AL-2-long
2	1841	75.1	340	2	AAW31544	Aaw31544 Human cyt
3	1841	75.1	340	2	AAW33699	Aaw33699 AL-2-shor
4	1841	75.1	340	2	AAW10637	Aaw10637 NLERK2 li
5	1841	75.1	340	6	ABU07845	Abu07845 Human eph
6	1841	75.1	340	8	ADQ21436	Adq21436 Human sof
7	1841	75.1	340	9	ADY51247	Ady51247 Human eph
8	1835	74.9	340	2	AAW17081	Aaw17081 EPH famil
9	1827	74.6	340	2	AAW46615	Aaw46615 Human tra
10	1771	72.3	340	6	ABU07846	Abu07846 Mouse eph
11	1771	72.3	340	9	ADY51239	Ady51239 Mouse eph
12	1550	63.3	285	7	ADJ70889	Adj70889 Human hea
13	628.5	25.7	334	2	AAW00287	Aaw00287 Mouse Eph
14	628.5	25.7	336	2	AAR92742	Aar92742 Murine he
15	626.5	25.7	336	9	ADY51238	Ady51238 Mouse eph
16	626.5	25.6	336	6	ABU07844	Abu07844 Mouse eph
17	623	25.4	346	2	AAR55059	Aar55059 Elk tyros
18	623	25.4	346	2	AAR91930	Aar91930 Human cyt
19	623	25.4	346	2	AAW19249	Aaw19249 Human elk
20	623	25.4	346	2	AAW36055	Aaw36055 Human elk
21	623	25.4	346	6	ABU07841	Abu07841 Human eph
22	623	25.4	346	6	ABU62401	Abu62401 Human elk
23	623	25.4	346	6	ABU62401	Abu62401 Human eph
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25	623	25.4	346	8	ADH76244	Adh76244 Human nov
26	623	25.4	346	8	ADO28631	Ado28631 Chicken E
27	623	25.4	346	8	ADR73462	Adr73462 Human Epr
28	623	25.4	346	9	ADV97175	Adv97175 Human eph
29	623	25.4	346	9	ADY51245	Ady51245 Human eph
30	622	25.4	346	2	AAR82606	Aar82606 Eph trans
31	621.5	25.4	331	2	AAW00288	Aaw00288 Chicken E
32	620.5	25.3	333	2	AAR94655	Aar94655 Ligand fo
33	620.5	25.3	333	2	AAR92743	Aar92743 Human hep
34	620.5	25.3	333	2	AAR89287	Aar89287 Human LER
35	620.5	25.3	333	2	AAW06337	Aaw06337 Full leng
36	620.5	25.3	333	2	AAW11308	Aaw11308 Receptor-
37	620.5	25.3	333	6	ABU07886	Abu07886 Novel hum
38	620.5	25.3	333	7	ADD89059	Add89059 TAT245. 1
39	620.5	25.3	333	8	ADN03886	Adn03886 Antipsori
40	620.5	25.3	333	8	ADP26886	Adp26886 Human Eph
41	620.5	25.3	333	8	ADR67298	Adr67298 Human bla
42	620.5	25.3	333	8	ADR86706	Adr86706 Human Eph
43	620.5	25.3	333	8	ADR82653	Adr82653 Human Eph
44	620.5	25.3	333	9	ADV73221	Adv73221 Human col
45	620.5	25.3	333	9	ADY51246	Ady51246 Human eph

ALIGNMENTS

RESULT 1
AAW33698
ID　AAW33698 standard; protein; 455 AA.
XX
AC　AAW33698;
XX
DT　30-APR-1998　(first entry)
XX
DE　AL-2-long (AL-2l) protein.
XX
KW　AL-21; AL-2; AL-2-long; human; treatment; neurological disorder; tumour;
KW　rheumatoid arthritis; wound healing; paralysis; angiogenesis; leukaemia;
KW　psoriasis; Alzheimer's disease; epilepsy.
XX
OS　Homo sapiens.
XX
FH
FT　Key　　　　　　Location/Qualifiers
FT
FT　Peptide　　　　1..26
FT　　　　　　　　/note= "signal peptide"
FT　Protein　　　　27..455
FT　　　　　　　　/note= "mature protein"
FT　Domain　　　　27..219
FT　　　　　　　　/note= "extracellular domain"
FT　Domain　　　　220..245
FT　　　　　　　　/note= "hydrophobic transmembrane domain"
XX
PN　WO9740153-A1.
XX
PD　30-OCT-1997.
XX
PF　17-APR-1997; 97WO-US006345.
XX
PR　19-APR-1996; 96US-00635130.
XX
PA　(GETH) GENENTECH INC.
XX
PI　Caras IW;
XX
DR　WPI; 1997-535837/49.
DR　N-PSDB; AAV06354.
XX
PT　Human AL-2 neurotrophic factor and related DNA - used to develop products
PT　for, e.g. treating neurologic disorders, angiogenesis disorders, tumours
PT　or rheumatoid arthritis or for wound healing.
XX
PS　Claim 20; Fig 1A-C; 86pp; English.

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.

CC   This is a AL-2-long (AL-2l) protein. The AL-2 is a novel Eph-related
CC   tyrosine kinase receptor ligand. AL-2 can be administered to patients in
CC   whom the nervous system has been damaged by trauma, surgery, stroke,
CC   ischaemia, infection, metabolic deficiency, nutritional deficiency,
CC   malignancy, or toxic agents, to promote the survival or growth of
CC   neurons. They can be used to treat motoneuron disorders such as
CC   amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, and
CC   various conditions involving spinal muscular atrophy, or paralysis. AL-2
CC   can be used to treat human neurodegenerative disorders, such as
CC   Alzheimer's disease, Parkinson's disease, epilepsy, demyelinating
CC   diseases such as multiple sclerosis, Huntingtons chorea, Down's syndrome,
CC   nerve deafness, Menier's disease, and other disorders of the cerebellum.
CC   AL-2 can be used as cognitive enhancer, to enhance learning particularly
CC   in dementias or trauma, since they can promote axonal outgrowth and
CC   synaptic plasticity, particularly of hippocampal neurons that express AL-
CC   2 binding Eph-family receptors and cortical neurons that express AL-2. AL
CC   -2 can also be used for wound healing, i.e. accelerating
CC   neovascularisation of, e.g. burns and ulcers. The encoding nucleic acids
CC   are useful in preparing antibodies that specifically bind to the AL-2
CC   protein. The antibodies and the AL-2 antagonists can be used in diagnosing
CC   and treating various neuronal disorders. AL-2 antagonists can be used for
CC   modulating angiogenesis. They can also be used for the treatment of
CC   tumours, acute myeloid leukaemia (AML), chronic myeloid leukaemia (CML),
CC   myelodysplastic syndrome (MDS), diabetic retinopathy, neovascular
CC   glaucoma, psoriasis and rheumatoid arthritis
XX
SQ   Sequence 455 AA;

Query Match             100.0%;  Score 2450; DB 2; Length 455;
Best Local Similarity   100.0%;  Pred. No. 3.6e-197;
Matches  455;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGPPHSGPGGVRVGALLLLGVLLGVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGPPHSGPGGVRVGALLLLGVLLGVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVCQSPRGGAVPRKP 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVCQSPRGGAVPRKP 180

Qy        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
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Db        181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy        241 GVAGAGGAMCWRRRARAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GVAGAGGAMCWRRRARAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy        301 GAADPPFCPHYEKVSGDYGHPVIVQDGPPQSPPNIYYTSISVLEWPILHTIQLFPMRSK 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAADPPFCPHYEKVSGDYGHPVIVQDGPPQSPPNIYYTSISVLEWPILHTIQLFPMRSK 360

Qy        361 CSRVTTFLFPVQVITTSTCRMTSFSFTTLNPSMQACRAQMGEFRIRWCFWGDRILGTALF 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CSRVTTFLFPVQVITTSTCRMTSFSFTTLNPSMQACRAQMGEFRIRWCFWGDRILGTALF 420

Qy        421 VLVLILLLGRLNMHQTTLLRQRASVEAEAGQHGPL 455
              |||||||||||||||||||||||||||||||||||
Db        421 VLVLILLLGRLNMHQTTLLRQRASVEAEAGQHGPL 455

RESULT 2
ID   AAW31544 standard; protein; 340 AA.
XX
AC   AAW31544;
XX
DT   14-APR-1998 (first entry)


DE   Human cytokine Lerk-8.
XX
KW   Lerk-8; cytokine; human; hek; elk; receptor tyrosine kinase; ligand;
KW   neurodegenerative disease; wound healing; neovascularisation; diagnosis;
KW   therapy.
XX
OS   Homo sapiens.
XX
Key           Location/Qualifiers
FH
FT   Peptide           1..27
FT                     /label= Sig_peptide
FT   Protein           28..340
FT                     /label= Mat_protein
FT   Domain            28..224
FT                     /note= "extracellular domain"
FT   Modified-site     210..212
FT                     /note= "N-glycosylated"
FT   Domain            225..251
FT                     /note= "transmembrane domain"
FT   Domain            252..340
FT                     /note= "cytoplasmic domain"
FT   Misc-difference   325
FT                     /note= "residue 325 is Leu in Lerk-8 variant"
XX
PN   WO9736919-A2.
XX
PD   09-OCT-1997.
XX
PF   19-MAR-1997; 97WO-US004533.
XX
PR   21-MAR-1996; 96US-00621146.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Cerretti DP;
XX
DR   WPI; 1997-503043/46.
DR   N-PSDB; AAT89519.
XX
PT   New isolated cytokine, Lerk-8 - binds to the hek and elk receptor
PT   tyrosine kinases, used to develop products for diagnosis and therapy.
XX
PS   Claim 3; Page 32-33; 37pp; English.

XX
CC   This protein sequence comprises a novel human cytokine designated Lerk-8.
CC   The amino acid sequence was deduced from a human foetal brain cDNA clone
CC   (see AAT89519). Lerk-8 binds to the cell surface receptors hek and elk,
CC   which are members of the eph/elk family of receptor tyrosine kinases.
CC   Lerk-8 polypeptides, especially soluble polypeptides comprising amino
CC   acid residues -27 to 142-197 of the full-length protein, can be expressed
CC   in transformed host cells. These polypeptides can be used to purify hek
CC   or elk proteins, and to purify or identify cells that express hek or elk
CC   on the surface. Such cells can be used in various in vitro studies or in
CC   vivo procedures, e.g. neural cells expressing elk can be administered to
CC   a mammal afflicted with a neurodegenerative disorder. The Lerk-8
CC   polypeptides can also be used to deliver diagnostic or therapeutic agents
CC   to these cells (e.g. leukaemia cells). The Lerk-8 DNA and polypeptides
CC   can also be used to: treat disorders mediated by defective or
CC   insufficient amounts of Lerk-8; to treat disorders such as injury to
CC   neural tissue or neurologic disease; to promote angiogenesis; and for
CC   wound healing or stimulating neovascularisation of grafted tissues
XX
SQ   Sequence 340 AA;

Query Match             75.1%;  Score 1841; DB 2; Length 340;
Best Local Similarity   75.1%;  Pred. No. 4.1e-146;
Matches  338;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGPPHSGPGGVRVGALLLLGVLLGVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGPPHSGPGGVRVGALLLLGVLLGVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
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RESULT 3

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ID   AAW33699 standard; protein; 340 AA.
XX
AC   AAW33699;
XX
DT   30-APR-1998 (first entry)
XX
DE   AL-2-short (AL-2s) protein.
XX
KW   AL-2s; AL-2; AL-2-short; human; treatment; neurological disorder; tumour;
KW   rheumatoid arthritis; wound healing; paralysis; angiogenesis; leukaemia;
KW   psoriasis; Alzheimer's disease; epilepsy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..26
FT                   /notes= "signal peptide"
FT   Protein         27..340
FT                   /notes= "mature protein"
FT   Domain          27..219
FT                   /notes= "extracellular domain"
FT   Domain          220..245
FT                   /notes= "hydrophobic transmembrane domain"
XX
PN   WO9740153-A1.
XX
PD   30-OCT-1997.
XX
PF   17-APR-1997; 97WO-US006345.
XX
PR   19-APR-1996; 96US-00635130.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Caras IW;
XX
DR   WPI; 1997-535837/49.
DR   N-PSDB; AAV06355.
XX
PT   Human AL-2 neurotrophic factor and related DNA - used to develop products
PT   for, e.g. treating neurologic disorders, angiogenesis disorders, tumours
PT   or rheumatoid arthritis or for wound healing.
XX
PS   Claim 20; Fig 2A-B; 86pp; English.
XX
CC   This is a AL-2-short (AL-2s) protein. The AL-2 is a novel Eph-related
CC   tyrosine kinase receptor ligand. AL-2 can be administered to patients in
CC   whom the nervous system has been damaged by trauma, surgery, stroke,
CC   ischaemia, infection, metabolic disease, nutritional deficiency,
CC   malignancy, or toxic agents, to promote the survival or growth of
CC   neurons. They can be used to treat motoneuron disorders such as
```

```
Qy   61 LCPRARPGPHSSPNYEFYKLIVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
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Qy  181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAGGLALLLL 240
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Qy  301 GAADPPFCPHYEKVSGDYGHPVIVQDGPPQSPPNIIY 338
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RESULT 4

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ID   AAW10637 standard; protein; 340 AA.
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AC   AAW10637;
XX
DT   23-JUN-1997 (first entry)
XX
DE   NLERK2 ligand for eph-related kinase.
XX
KW   LERK; ligand for eph-related kinase; ERK; NLERK2;
KW   receptor protein tyrosine kinase; cell proliferation;
KW   cell differentiation; cell survival; nerve cell.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..29
FT                   /label= Sig_peptide
FT   Protein         30..340
FT                   /label= Mat_protein
FT   Modified-site   210
FT                   /label= ...
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Query Match             75.1%;  Score 1841;  DB 2;  Length 340;
Best Local Similarity   100.0%;   Pred. No. 4.1e-146;
Matches  338;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
Qy   61 LCPRARPGPHSSPNYEFYKLIVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
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Qy  121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQQGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
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Db  121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQQGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
Qy  181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAGGLALLLL 240
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Db  181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAGGLALLLL 240
Qy  241 GVAGAGGAMCWRRRARKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG 300
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Db  241 GVAGAGGAMCWRRRARKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG 300
Qy  301 GAADPPFCPHYEKVSGDYGHPVIVQDGPPQSPPNIIY 338
         |||||||||||||||||||||||||||||||||||||
Db  301 GAADPPFCPHYEKVSGDYGHPVIVQDGPPQSPPNIIY 338
```

```
CC   amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, and
CC   various conditions involving spinal muscular atrophy, or paralysis. AL-2
CC   can be used to treat human neurodegenerative disorders, such as
CC   Alzheimer's disease, Parkinson's disease, epilepsy, demyelinating
CC   diseases such as multiple sclerosis, Huntingtons chorea, Down's syndrome,
CC   nerve deafness, Menier's disease, and other disorders of the cerebellum.
CC   AL-2 can be used as cognitive enhancer, to enhance learning particularly
CC   in dementias or trauma, since they can promote axonal outgrowth and
CC   synaptic plasticity, particularly of hippocampal neurons that express AL-
CC   2 binding Eph-family receptors and cortical neurons that express AL-2. AL
CC   -2 can also be used for wound healing, i.e. accelerating
CC   neovascularisation of, e.g. burns and ulcers. The encoding nucleic acids
CC   are useful in preparing antibodies that specifically bind to the AL-2
CC   protein. The antibodies and the AL-2 antagonists are useful in diagnosing
CC   and treating various neuronal disorders. AL-2 antagonists can be used for
CC   modulating angiogenesis. They can also be used for the treatment of
CC   tumours, acute myeloid leukaemia (AML), chronic myeloid leukaemia (CML),
CC   myelodysplastic syndrome (MDS), diabetic retinopathy, neovascular
CC   glaucoma, psoriasis and rheumatoid arthritis
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SQ   Sequence 340 AA;
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PF   19-JUL-1996;   96WO-AU00460.
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PR   20-JUL-1995;   95AU-0004004263.
PR   27-NOV-1995;   95AU-00008847.
PR   22-DEC-1995;   95AU-00007299.
PR   05-FEB-1996;   96AU-00007890.
XX
PA   (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI   Nicola NA;
XX
DR   WPI; 1997-132632/12.
DR   N-PSDB; AAT60966.
XX
PS   Claim 16; Page 37-39; 71pp; English.
XX
CC   A novel human ligand for eph-related kinase (LERK) is designated NLERK2
CC   (AAW10637). It is encoded by a cDNA clone (AAT60966) obtd. from a human
CC   foetal brain cDNA library. The novel receptor ligand can be expressed in
CC   transformed host cells and used in methods for regulating the
CC   development, maintenance or regeneration of different cells (e.g.
CC   neurons) and tissues in vivo and in vitro. Soluble NLERK2 peptides can be
CC   used to treat injury, disease or abnormality in the nervous system, and
CC   membrane-bound NLERK2 to modulate proliferation, different or survival
CC   e.g. in grafting procedures or transplantation. NLERK2 can also be used
CC   to raise antibodies for use in immunotherapy, and to detect anti-NLERK2
CC   antibodies that may occur in some autoimmune diseases
XX
SQ   Sequence 340 AA;

Query Match   75.1%; Score 1841; DB 2; Length 340;
Best Local Similarity   100.0%; Pred. No. 4.1e-146;
Matches 338; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy   61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

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Db   241 GVAGAGGAMCWRRRARXPSESRHPGCSFGRGSLGLGGGGMGPREABPGELGIALRGG 300

Qy   301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYY 338
               |||||||||||||||||||||||||||||||||||
Db   301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYY 338

ID   ABU07845 standard; protein; 340 AA.
XX
AC   ABU07845;
XX
DT   10-MAY-2003 (first entry)
XX
DE   Human ephrin-B3 ligand.
XX
KW   Cytostatic; vasodilator; antiinflammatory; cardiant; gene therapy;
KW   ligand-receptor binding modulator; ephrin ligand; angiogenesis;
KW   lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;
KW   cell migration disorder; cell proliferation disorder; neovascularisation;
KW   ischaemia; infarction; tissue graft; transplant; human; ephrin-B3;
KW   tie receptor tyrosine kinase; Eph receptor ligand.
XX
OS   Homo sapiens.
XX
PN   WO200300045529-A2.
XX
PD   16-JAN-2003.
XX
PF   02-JUL-2002;   2002WO-IB002524.
XX
PR   02-JUL-2001;   2001US-0302960P.
XX
PA   (LICN) LICENTIA LTD.
XX
PI   Alitalo K, Kubo H;
XX
DR   WPI; 2003-210341/20.
DR   N-PSDB; ABX12546.
XX
PS   Disclosure; Page 117-119; 199pp; English.
XX
CC   The invention describes a method of identifying a modulator of binding
CC   between a Tie receptor tyrosine kinase and an Ephrin ligand. The method
CC   comprises contacting a Tie receptor composition with an Ephrin
CC   composition in the presence and in the absence of a putative modulator
CC   compound, and detecting the binding between Tie receptor and the Ephrin
CC   in the presence and in the absence of the putative modulator. The receptor
CC   is useful for identifying a modulator of binding between a Tie receptor
CC   tyrosine kinase and an Ephrin ligand. Modulators identified from the
CC   method are useful in modulating angiogenic processes, including
CC   lymphangiogenesis, for treating diseases associated with aberrant Ephrin-
CC   Tie biology, aberrant growth, migration or proliferation of cells that
CC   express a Tie receptor, or for promoting growth of vessel or
CC   neovascularisation (e.g. ischaemic tissue, an infarction, a new or
CC   chronic compound, or a tissue graft or transplant). This is the amino
CC   acid sequence of human Ephrin-B3, a member of the Ephrin-B subclass of
CC   ligands that are bound to the membrane via a transmembrane domain and
CC   short cytoplasmic tail and function as Eph receptor ligands
XX
SQ   Sequence 340 AA;

Query Match   75.1%; Score 1841; DB 6; Length 340;
Best Local Similarity   100.0%; Pred. No. 4.1e-146;
Matches 338; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy   61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy   181 VSEMPEMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 VSEMPEMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy   241 GVAGAGGAGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GVAGAGGAGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy   301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIIY 338
           |||||||||||||||||||||||||||||||||||||
Db   301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIIY 338

RESULT 6
ID   ADQ21436 standard; protein; 340 AA.
XX
AC   ADQ21436;
XX
DT   26-AUG-2004 (first entry)
XX
DE   Human soft tissue sarcoma-upregulated protein - SEQ ID 4256.
XX
KW   soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX
OS   Homo sapiens.
XX
XX
PN   WO200048938-A2.
XX
PD   10-JUN-2004.
XX
PF   26-NOV-2003; 2003WO-US038193.
XX
PR   26-NOV-2002; 2002US-0429739P.
XX
PA   (PROT-) PROTEIN DESIGN LABS INC.
XX
PI   Aziz N, Ginsburg WM, Zlotnik A;
XX
DR   WPI; 2004-441208/41.
XX
XX
PT   Example 2; SEQ ID NO 4256; English.
XX
PT   Early detection of soft tissue sarcoma comprises determining expression
PT   of a gene in a first soft tissue sample and a normal soft tissue sample
PT   and comparing the gene expression, also useful in treating soft tissue
PT   sarcoma.
CC
CC   The invention relates to a novel method for detecting soft tissue sarcoma
CC   which comprises obtaining a first soft tissue sample from an individual,
CC   and a normal soft tissue sample from the same or different individual,
CC   determining the expression of a gene in both samples and comparing the
CC   expression of the gene in the first soft tissue samples, where a higher level
CC   of protein expression in the first soft tissue sample indicates the
CC   presence of soft tissue sarcoma. The method of the invention has
CC   cytostatic applications and may be useful for detecting soft tissue
CC   sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC   acid sequences may be useful in diagnostic and screening applications.
CC   The current sequence is that of a human soft tissue sarcoma-upregulated
CC   protein of the invention. The current sequence is not shown within the
CC   specification per se but was submitted in CD format by the inventor.
XX
XX
SQ   Sequence 340 AA;

Qy   Query Match   75.1%; Score 1841; DB 8; Length 340;
      Best Local Similarity 100.0%; Pred. No. 4.1e-146;
      Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL   60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL   60

Qy   61 LCPRARPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LCPRARPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy   181 VSEMPEMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL 240
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 VSEMPEMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL 240

Qy   241 GVAGAGGAGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GVAGAGGAGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy   301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIIY 338
           ||||||||||||||||||||||||||||||||||||||
Db   301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIIY 338

RESULT 7
ID   ADY51247 standard; protein; 340 AA.
XX
AC   ADY51247;
XX
DT   19-MAY-2005 (first entry)
XX
DE   Human ephrin-B3 SEQ ID NO:16.
XX
KW   ephrin; hematopoiesis; hyperproliferation; cytostatic; antianemic;
KW   antiinflammatory; antipsoriatic; gastrointestinal-gen.; dermatological;
KW   coagulant; immunostimulant; cerebroprotective; vasotropic; antiulcer.
XX
OS   Homo sapiens.
XX
XX
PN   US2005049194-A1.
XX
PD   03-MAR-2005.
XX
PF   31-OCT-2003; 2003US-00698907.
XX
PR   09-NOV-2001; 2001US-0345206P.
PR   02-JUL-2002; 2002US-0393272P.
PR   08-NOV-2002; 2002US-00291290.
PR   03-APR-2003; 2003US-0464088P.
XX
PA   (FRIS/) FRISEN J.
PA   (HOLM/) HOLMBERG J.
XX
PI   Frisen J, Holmberg J;
XX
DR   WPI; 2005-195317/20.
XX
XX
PT   Disclosure; SEQ ID NO 16; 68pp; English.
XX
PT   Use of ephrin and its molecules for alleviating a symptom or a disorder
PT   with reduced levels of hematopoiesis, increased levels of cellular
PT   proliferation in an intestinal tract, or abnormal level of cellular
PT   proliferation in a tissue.
XX
CC   The invention relates to a novel use of ephrin, ephrin inhibitors, and
CC   ephrin receptors for alleviating a symptom of a disorder having reduced
CC   levels of hematopoiesis, having increased levels of cellular
CC   proliferation in an intestinal tract, or having an abnormal level of
CC   cellular proliferation in a tissue. A composition of the invention has
CC   cytostatic, antianemic, antiinflammatory, antipsoriatic, gastrointestinal
CC   -gen., dermatological, coagulant, immunostimulant, cerebroprotective,
CC   vasotropic, and antiulcer activity. The present sequence represents
CC   murine ephrin-B3.
XX

Qy   301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIIY 338

Db   301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIIY 338

Qy   241 GVAGAGGAGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Db   241 GVAGAGGAGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy   181 VSEMPEMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL 240

Db   181 VSEMPEMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL 240

Qy   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Db   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy   61 LCPRARPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Db   61 LCPRARPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

SQ   Sequence 340 AA;

Qy   Query Match   75.1%; Score 1841; DB 9; Length 340;
     Best Local Similarity   100.0%; Pred. No. 4.1e-146;
Matches 338; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPYWNSANKRFQAEGGYVLYPQIGDRLDL 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy   61 LCPRARPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LCPRARPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy   181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy   241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSSLGLGGGGGMGPREAEPGELGIALRGG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy   301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYY 338
          ||||||||||||||||||||||||||||||||||||||
Db   301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYY 338

RESULT 8
AAW17081
ID   AAW17081 standard; protein; 340 AA.
XX
AC   AAW17081;
XX
DT   09-AUG-1997 (first entry)
XX
DE   EPH family ligand Efl-6.
XX
KW   Efl-6; Eph; Elk; receptor tyrosine kinase; signal transduction; ligand;
KW   neurological disease.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FH
FT   Peptide   1..24
FT   /label= Sig_peptide
FT   Protein   25..340
FT   /label= Mat_protein
FT   Misc-difference 166
FT   /label= Gln, Arg
FT   Domain   225..249
FT   /label= Transmembrane_domain
XX
PN   WO9715667-A1.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996; 96WO-US017201.
XX
PR   25-OCT-1995; 95US-0007015P.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Davis S, Gale NW, Yancopoulos GD;
XX
DR   WPI; 1997-259021/23.
DR   N-PSDB; AAT69808.
XX
PT   New nucleic acid encoding Efl-6 ligand protein - used for promoting
PT   growth and proliferation of neuronal cells and in drug screening.

XX
PN   Claim 2; Fig 1; 36pp; English.
XX
PS
CC   A novel ligand (AAW17081), designated Efl-6 (or Eph transmembrane
CC   tyrosine kinase family ligand 6), binds to the Elk, Nuk/Cek5, Hek2/Sek4,
CC   Htk and Sek1 receptors on cells. Its amino acid sequence was deduced from
CC   a human frontal cortex cDNA clone (AAT69808). Recombinant Elf-6,
CC   truncated soluble polypeptides comprising the extracellular domain of Elf
CC   -6, and Elf-6 ligandbodies comprising soluble Efl-6 and the Fc portion of
CC   IgG can be expressed in host cells. These can be used to support neuronal
CC   and other Eph receptor-bearing cell populations for treatment of
CC   neurological disorders, in drug screening and to raise diagnostic
CC   antibodies.
XX
SQ   Sequence 340 AA;

Qy   Query Match   74.9%; Score 1835; DB 2; Length 340;
     Best Local Similarity   99.7%; Pred. No. 1.1e-145;
Matches 337; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPYWNSANKRFQAEGGYVLYPQIGDRLDL 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy   61 LCPRARPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LCPRARPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy   181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy   241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSSLGLGGGGGMGPREAEPGELGIALRGG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy   301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYY 338
          ||||||||||||||||||||||||||||||||||||||
Db   301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYY 338

RESULT 9
AAW46615
ID   AAW46615 standard; protein; 340 AA.
XX
AC   AAW46615;
XX
DT   06-JUL-1998 (first entry)
XX
DE   Human transmembrane ligand Elk-L3.
XX
KW   Elk-L3; Elk-related receptor tyrosine kinase; transmembrane ligand;
KW   human; signal transduction; axonogenesis; nerve cell; neurone;
KW   Alzheimer's disease; Parkinson's disease; Huntingdon's disease;
KW   demyelination; multiple sclerosis; amyotrophic lateral sclerosis;
KW   nervous system infection; Wernicke's disease; trauma; ischaemia; stroke;
KW   nutritional polyneuropathy; progressive supranuclear palsy;
KW   Shy Drager's syndrome; multisystem degeneration;
KW   olivo ponto cerebellar atrophy, peripheral nerve damage.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FH
FT   Misc-difference 166
FT   /label= Gln, Arg
FT   Domain   225..249
FT   /note= "transmembrane domain"
XX
PN   WO9801548-A1.

```
XX
PD   15-JAN-1998.
XX
PF   04-JUL-1997;   97WO-CA000473.
XX
PR   05-JUL-1996;   96US-0021272P.
XX
PA   (MOUN ) MOUNT SINAI HOSPITAL CORP.
XX
PI   Holland S, Mbamalu G, Pawson T;
XX
DR   WPI; 1998-101047/09.
DR   N-PSDB; AAV16097.
XX
PS   Disclosure; Fig 5A; 40pp; English.
XX
PT   This polypeptide comprises human Elk-L3, a transmembrane ligand of Elk-
CC   related receptor tyrosine kinase (ERRTK). A novel method of modulating
CC   the biological activity of, or for affecting a pathway regulated by, a
CC   transmembrane ligand for an ERRTK in a cell expressing the transmembrane
CC   ligand comprises forming a complex between a purified and isolated
CC   oligomerised ERRTK, or an isoform or an extracellular domain of the
CC   ERRTK, and the transmembrane ligand expressed on the cell. The complex
CC   can also be used for evaluating a substance for its ability to modulate
CC   the biological activity of a transmembrane ligand for an ERRTK, and to
CC   identify substances that affect or modulate a pathway regulated by a
CC   ERRTK. A purified and isolated oligomerised ERRTK can be used in the
CC   preparation of a medicament for modulating neuronal development or
CC   regeneration in a subject, or in a medicament for modulating axonogenesis
CC   in a subject (all claimed). The substances identified by the methods can
CC   be used to modulate axonogenesis, nerve cell interactions and
CC   regeneration, to treat diseases and conditions involving trauma and
CC   injury to the nervous system, such as Alzheimer's disease, Parkinson's
CC   disease, Huntingdon's disease, demyelinating diseases, such as multiple
CC   sclerosis, amyotrophic lateral sclerosis, bacterial and viral infections
CC   of the nervous system, deficiency diseases, such as Wernicke's disease
CC   and nutritional polyneuropathy, progressive supranuclear palsy, Shy
CC   Drager's syndrome, multisystem degeneration and olivo ponto cerebellar
CC   atrophy, peripheral nerve damage, trauma, and ischaemia resulting from
CC   stroke
XX
SQ   Sequence 340 AA;

Query Match          74.6%;   Score 1827;  DB 2;  Length 340;
Best Local Similarity  99.4%;  Pred. No. 6.2e-145;
Matches 336;  Conservative  0;  Mismatches  2;  Indels  0;  Gaps  0;

Qy     1  MGPPHSGPGGVRVGALLLLGVLGVLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL  60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1  MGPPHSGPGGVRVGALLLLGVLGVLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL  60

Qy    61  LCPRARPPGPHSSPNYEYRKLYLVGGAQGRRCEAPPAPANLLLTCDRPDLDLRFTIKFQEY 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61  LCPRARPPGPHSSPNYEFRKLYLVGGAQGRRCEAPPAPANLLLTCDRPDLDLRFTIKFQEY 120

Qy   121  SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  SPNLWGHEFRSHHDYYIATSDGTREGLESLQGGVCLTRGMKVLLXVGQSPRGGAVPRKP   180

Qy   181  VSEMPMERDRGAAHSLEPGKENLPGDFTPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  VSEMPMERDRGAAHSLEPCKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL  240

Qy   241  GVAGAGGAMCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  GVAGAGGAMCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG  300

Qy   301  GAADPPFCPHYEKVSGDYGHPVYIVQDGPPPQSPQNIYY  338
          |||||||||||||||||||||||||||||||||||||||
Db   301  GAADPPFCPHYEKVSGDYGHPVVIVQDGPPPQSPNIYY   338
```

```
Db   301  GAADPPFCPHYEKVSGDYGHPVVIVQDGPPPQSPQNIYY  338

RESULT 10
ABU07846
ID   ABU07846 standard; protein; 340 AA.
XX
AC   ABU07846;
XX
DT   10-MAY-2003  (first entry)
XX
DE   Mouse ephrin-B3 ligand.
XX
KW   Cytostatic; vasodilator; antiinflammatory; cardiant; gene therapy;
KW   ligand-receptor binding modulator; ephrin ligand; angiogenesis;
KW   lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;
KW   cell migration disorder; cell proliferation disorder; neovascularisation;
KW   ischaemia; infarction; tissue graft; transplant; mouse; ephrin-B3;
KW   Tie receptor tyrosine kinase; Eph receptor ligand.
XX
OS   Mus musculus.
XX
PN   WO200300454529-A2.
XX
PD   16-JAN-2003.
XX
PF   02-JUL-2002;   2002WO-IB002524.
XX
PR   02-JUL-2001;   2001US-0302960P.
XX
PA   (LICN ) LICENTIA LTD.
XX
PI   Alitalo K, Kubo H;
XX
DR   WPI; 2003-210341/20.
DR   N-PSDB; ABX12547.
XX
PS   Disclosure; Page 121-122; 199pp; English.
XX
PT   Identifying modulators of binding between a Tie receptor tyrosine kinase
PT   and an Ephrin ligand, useful for promoting neovascularization, comprises
CC   contacting a Tie receptor with an Ephrin in the presence of a putative
CC   modulator.
XX
CC   The invention describes a method of identifying a modulator of binding
CC   between a Tie receptor tyrosine kinase and an Ephrin ligand. The method
CC   comprises contacting a Tie receptor composition with an Ephrin
CC   composition in the presence and in the absence of a putative modulator
CC   compound, and detecting the binding between Tie receptor and the Ephrin
CC   in the presence and in the absence of the putative modulator. The method
CC   is useful for identifying a modulator of binding between a Tie receptor
CC   tyrosine kinase and an Ephrin ligand. Modulators identified from the
CC   method are useful in modulating angiogenic processes, including
CC   lymphangiogenesis, for treating diseases associated with aberrant Ephrin-
CC   Tie biology, aberrant growth, migration or proliferation of cells that
CC   express a Tie receptor, or for promoting growth of vessel or
CC   neovascularisation (e.g. ischaemic tissue, an infarction, a new or
CC   chronic compound, or a tissue graft or transplant). This is the amino
CC   acid sequence of mouse Ephrin-B3, a member of the Ephrin-B subclass of
CC   ligands that are bound to the membrane via a transmembrane domain and
CC   short cytoplasmic tail and function as Eph receptor ligands
XX
SQ   Sequence 340 AA;

Query Match          72.3%;   Score 1771;  DB 6;  Length 340;
Best Local Similarity  95.6%;  Pred. No. 3.2e-140;
Matches 323;  Conservative  7;  Mismatches  8;  Indels  0;  Gaps  0;

Qy     1  MGPPHSGPGGVRVGALLLLGVLGVLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL  60
          ||  || ||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db     1  MGAPHFGPGGVQVGALLLLGFAGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL   60

Qy    61  LCPRARPPGPHSSPNYEYRKLYLVGGAQGRRCEAPPAPANLLLTCDRPDLDLRFTIKFQEY 120
```

```
Db      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   61 LCPRARPPGPHSSSPSYEFYKLYLVEGAQQRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
Db   61 LCPRARPPGPHSSSPSYEFYKLYLVEGAQQRRCEAPPAPNLLLTCDRPDLDLRFIKFQEY  120
Qy  121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP  180
Db  121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP  180
Qy  181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL  240
Db  181 VSEMPMERDRGAAHSAEPGRDTIPGDPSSNATSRGAEGPLPPPSMPAVAGAAGGMALLLL  240
Qy  241 GVAGAGGAMCWRRRRAKPSESRHPGPGSPGRGGSSLGLGGGGGMGPREAEPGELGIALRGG 300
Db  241 GVAGAGGAMCWRRRRAKPSESRIPGPGSFGRGGSSLGLGGGGGMGPREAEPGELGIALRGG 300
Qy  301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIY 338
Db  301 GTADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIY 338
```

RESULT 11
ADY51239

```
ID   ADY51239 standard; protein; 340 AA.
XX
AC   ADY51239;
XX
DT   19-MAY-2005  (first entry)
XX
DE   Mouse ephrin-B3 SEQ ID NO:8.
XX
OS   Mus musculus.
XX
KW   ephrin; hematopoiesis; hyperproliferation; cytostatic; antianemic;
KW   antiinflammatory; antipsoriatic; gastrointestinal-gen.; dermatological;
KW   coagulant; immunostimulant; cerebroprotective; vasotropic; antiulcer.
XX
PN   US2005049194-A1.
XX
PD   03-MAR-2005.
XX
PF   31-OCT-2003; 2003US-00698907.
XX
PR   09-NOV-2001; 2001US-0345206P.
PR   02-JUL-2002; 2002US-0393272P.
PR   08-NOV-2002; 2002US-00291290.
PR   03-APR-2003; 2003US-0460488P.
XX
PS   Disclosure; SEQ ID NO 8; 68pp; English.
XX
PI   Frisen J, Holmberg J;
XX
PA   (FRIS/) FRISEN J.
PA   (HOLM/) HOLMBERG J.
XX
DR   WPI; 2005-195317/20.
XX
CC   The invention relates to a novel use of ephrin, ephrin inhibitors, and
CC   ephrin receptors for alleviating a symptom of a disorder having reduced
CC   levels of hematopoiesis, having increased levels of cellular
CC   proliferation in an intestinal tract, or having an abnormal level of
CC   cellular proliferation in a tissue. A composition of the invention has
CC   cytostatic, antianemic, antiinflammatory, antipsoriatic, gastrointestinal
CC   -gen., dermatological, coagulant, immunostimulant, cerebroprotective,
CC   vasotropic, and antiulcer activity. The present sequence represents
CC   murine ephrin-B3.
XX
SQ   Sequence 340 AA;
```

Query Match 72.3%; Score 1771; DB 9; Length 340;
Best Local Similarity 95.6%;
Matches 323; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

```
Qy    1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQABGGYVLYPQIGDRLDL  60
Db    1 MGAPHFGPGGVQVGALLLLGFAGLVSGLSLEBPVYWNSANKRFQABGGYVLYPQIGDRLDL 60
Qy   61 LCPRARPPGPHSSSPSYEFYKLYLVEGAQQRRCEAPPAPNLLLTCDRPDLDLRFIKFQEY  120
Db   61 LCPRARPPGPHSSSPSYEFYKLYLVEGAQQRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
Qy  121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP  180
Db  121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP  180
Qy  181 VSEMPMERDRGAAHSAEPGRDTIPGDPSSNATSRGAEGPLPPPSMPAVAGAAGGMALLLL  240
Db  181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL  240
Qy  241 GVAGAGGAMCWRRRRAKPSESRHPGPGSPGRGGSSLGLGGGGGMGPREAEPGELGIALRGG 300
Db  241 GVAGAGGAMCWRRRRAKPSESRIPGPGSFGRGGSSLGLGGGGGMGPREAEPGELGIALRGG 300
Qy  301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIY 338
Db  301 GTADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIY 338
```

RESULT 12
ADJ70889

```
ID   ADJ70889 standard; protein; 285 AA.
XX
AC   ADJ70889;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human heat mitochondrial protein as a therapeutic target SeqID2695.
XX
OS   Homo sapiens.
XX
KW   mitochondrial; human; screening assay; diabetes mellitus;
KW   Huntington's disease; osteoarthritis;
KW   Leber's hereditary optic neuropathy; LHON;
KW   mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW   myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW   neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW   osteopathic; ophthalmological; cytostatic.
XX
PN   WO2003087768-A2.
XX
PD   23-OCT-2003.
XX
PF   04-APR-2003; 2003WO-US010870.
XX
PR   12-APR-2002; 2002US-0372843P.
PR   17-JUN-2002; 2002US-0389987P.
PR   20-SEP-2002; 2002US-0412418P.
XX
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
XX
PI   Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI   Warnock DE;
XX
DR   WPI; 2003-845369/78.
XX
CC   Identifying a mitochondrial target for drug screening assays and for
CC   treating diseases associated with altered mitochondrial function,
CC   comprises detecting a modified polypeptide in a sample and correlating
CC   with the disease.
XX
PS   Claim 1; SEQ ID NO 2695; 180pp; English.
```

```
XX
CC   This invention relates to novel mitochondrial targets that can be used
CC   for therapeutic intervention in treating a disease associated with
CC   altered mitochondrial function. Specifically, it refers to a method for
CC   identifying proteins of the human heart mitochondrial proteome that are
CC   useful for drug screening assays, as well as therapeutic targets. The
CC   present invention describes a method for identifying such proteins that
CC   can be used in the treatment of various diseases associated with altered
CC   mitochondrial function including diabetes mellitus, Huntington's disease,
CC   osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC   encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC   ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC   compositions have neuroprotective, nootropic, antidiabetic,
CC   anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC   cytostatic activities. This polypeptide sequence is a human heart
CC   mitochondrial protein of the invention.
XX
SQ   Sequence 285 AA;

Query Match     63.3%;  Score 1550;  DB 7;  Length 285;
Best Local Similarity  100.0%;
Matches  283;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy   56 DRLDLLCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTI 115
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 DRLDLLCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTI 60

Qy  116 KFQEYSPNLWGHEFRSHHDYYIIATSDGTGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGA 175
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 KFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGA 120

Qy  176 VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPPTSNATSRGAEGPLPPPSMPAVAGAAGGL 235
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPPTSNATSRGAEGPLPPPSMPAVAGAAGGL 180

Qy  236 ALLLLGVAGAGGAMCWRRRRAXPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGI 295
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ALLLLGVAGAGGAMCWRRRRAXPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGI 240

Qy  296 ALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIIY 338
         ||||||||||||||||||||||||||||||||||||||||||||
Db  241 ALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIIY 283


RESULT 13
ID   AAW00287 standard; protein; 334 AA.
AC   AAW00287;
XX
DT   19-JAN-1997  (first entry)
XX
DE   Mouse Eph receptor ligand ELF-2.
XX
KW   Eph receptor; ligand; ELF-2; tyrosine kinase; signal transduction;
KW   organogenesis; oncogenesis; tumour; neurological disorder; diagnosis;
KW   gene therapy.
OS   Mus sp.
XX
FH   Key             Location/Qualifiers
FT   Domain          1..224
FT                   /label= Extracellular_domain
FT   Binding-site    31..155
FT                   /label=Receptor_binding_site
FT   Domain          226..251
FT                   /label=Transmembrane_domain
XX
PN   WO9626958-A2.
XX
PD   06-SEP-1996.
XX
PF   23-FEB-1996; 96WO-US002673.
```

```
XX
PR   27-FEB-1995; 95US-00395415.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Flanagan JG, Bergemann AD;
XX
PT   WPI; 1996-433391/43.
PT   N-PSDB; AAT40230.
XX
PS   Claim 6; Fig 1A-B; 50pp; English.
XX
FT   Eph receptor ligand, ELF-2, and DNA encoding it - used to treat or
FT   prevent neurological diseases, and to modulate binding of ELF-2 to Eph
FT   receptor, e.g. to prevent or treat tumour formation.
XX
CC   Mouse Eph receptor ligand ELF-2 (AAW00287) is strongly expressed in the
CC   anterior hindbrain and newly-forming somites of embryos at the early
CC   organogenesis stage of development. It is important in cellular
CC   communication during pattern formation. Its amino acid sequence was
CC   deduced from a cDNA clone (AAT40230) isolated from a newborn mouse brain
CC   cDNA library. The ELF-2 ligand can be used to alter neurological
CC   development, oncogenesis and growth regulation, to modulate binding of
CC   ELF-2 to the Eph receptor, and in diagnostic assays
XX
SQ   Sequence 334 AA;

Query Match     25.7%;  Score 628.5;  DB 2;  Length 334;
Best Local Similarity  41.8%;  Pred No. 3.8e-44;
Matches  137;  Conservative  49;  Mismatches  129;  Indels  13;  Gaps  5;

Qy   14 GALILLIGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
         |:|:| |||||:|:|| :|||| : | :|||   |: :|||
Db   15 GLLMVLICRTAISRSIVLEPIYWNSSNSKFLPGGQLVLYPQIGDKLDIICPKV---DSKTV 71

Qy   74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
         ||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||| :|:
Db   72 GQYEYKVYVMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEBFSPNLWGLHFQKNK 131

Qy  134 DYYIIATSDGTGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
         :|:|| |:|||:.||||| |:||:|:| | |  :| ||  :.| :||:.||: :.
Db  132 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 191

Qy  191 GAAHSLEPGKENLPGDPPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
         : : : :|:
Db  192 GRSSTTSFPFVKPNPGSSTDGNSACHSGNGNNLLGSEVALFAGIASCGCIFIVIIITLVVLLL 251

Qy  251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
         |||| : |:
Db  252 KYRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEFSDVIIPLR---TADSVFCPH 304

Qy  311 YEKVSGDYGHPVYIVQDGPPQSPPNIIY 338
         ||||||||||||||||||||||||||||
Db  305 YEKVSGDYGHPVYIVQEMPQSPANIIY 332


RESULT 14
ID   AAR92742 standard; protein; 336 AA.
AC   AAR92742;
XX
DT   21-MAY-1996  (first entry)
XX
DE   Murine hepatoma transmembrane kinase receptor ligand.
XX
KW   Hepatoma transmembrane kinase; Htk; receptor; ligand; tyrosine kinase;
KW   neurodegenerative disease.
OS   Mus musculus.
XX
PN   WO9602645-A2.
XX
```

PD   01-FEB-1996.
XX
PF   14-JUL-1995;   95WO-US008812.
XX
PR   20-JUL-1994;   94US-00277722.
XX
PA   (GETH) GENENTECH INC.
XX
PI   Bennett BD, Matthews W;
XX
DR   WPI; 1996-105907/11.
DR   N-PSDB; AAT16470.
XX
PT   Ligand for the hepatoma trans-membrane kinase receptor - useful for
PT   stimulating and inhibiting cells carrying the receptor, e.g. for treating
PT   neuro-degenerative disease.
XX
PS   Claim 5; Fig 1(A-D); 88pp; English.
XX
CC   Mouse (AAT16470) and human (AAT16471) Htk ligand which bind to, and
CC   activate, the Htk receptor, have been identified in a variety of tissues
CC   using a soluble Htk-Fc fusion protein. The predicted mol.wt. of the
CC   murine Htk ligand protein following a signal peptide cleavage is 34 kd
CC   with an estimated pI of 8.9. The murine and human ligands show 96%
CC   homology at the amino acid level. The DNA is used to produce recombinant
CC   ligands; for tissue- specific typing (partic. as a marker for breast
CC   cancer) and as a marker for human chromosome 13. The ligands (partic. in
CC   soluble form) are used to activate the tyrosine kinase domain of the Htk
CC   receptor, i.e. to stimulate or inhibit growth, differentiation, and/or
CC   activation of cells contg. the receptor, e.g. treatment of
CC   neurodegenerative diseases, since they are strongly expressed in the
CC   cerebral cortex, hippocampus, striatum and cerebellum. The ligands are
CC   also useful as a control or standard in assays, for generation of
CC   antibodies, as a mol. wt. marker, for growth in vitro of Htk-receptor
CC   positive cells, as research agent, in screening, etc
XX
SQ   Sequence 336 AA;

Query Match   45.7%; Score 628.5; DB 2; Length 336;
Best Local Similarity   41.8%; Pred. No. 3.8e-44;
Matches 137; Conservative   49; Mismatches 129; Indels 13; Gaps   5;

Qy   14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVYLYPQIGDRLDLLCPRARPPGPHSS   73
              |::| |||||| :||||||||:||||:|||:|||||:|||:||||| ::
Db   17 GLIMVLCRTAISRSIVLEPIYWNSSNSKFLPGGLVLYPQIGDKLDIICPKV---DSKTV   73

Qy   74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
              |:| |||| |||||:| :||||| ||:| ||:|||||||:||||||||||:||||
Db   74 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQQNK 133

Qy   134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPER-DR 190
              ||||:| ::||| |||||:||||||||||||| |||||||:|||:||| ||
Db   134 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

Qy   191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
              |:||||| |||||| |||||:|:| |||| : ||:||:||| ||||||||||||:
Db   194 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVLLL 253

Qy   251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
              ||| :: ||| ::
Db   254 KYRRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH 306

Qy   311 YEKVSGDYGHPVYIVQDGPGGVIYY 338
              ||||:|||||||||: |: |||
Db   307 YEKVSGDYGHPVYIVQDMPPQQSPANIYY 334

DT   19-MAY-2005   (first entry)
XX
DE   Mouse ephrin-B2 SEQ ID NO:7.
XX
KW   ephrin; hematopoiesis; hyperproliferation; cytostatic; antianemic;
KW   antiinflammatory; antipsoriatic; gastrointestinal-gen.; dermatological;
KW   coagulant; immunostimulant; cerebroprotective; vasotropic; antiulcer.
XX
OS   Mus musculus.
XX
FH   Key   Location/Qualifiers
FT   Misc-difference 2..3
FT   /note= "Optionally deleted"
XX
XX
(FRIS/) FRISEN J.
(HOLM/) HOLMBERG J.
XX
PA   (FRIS/) FRISEN J.
PA   (HOLM/) HOLMBERG J.
XX
PI   Frisen J, Holmberg J;
XX
DR   WPI; 2005-195317/20.
XX
PN   US2005049194-A1.
XX
PD   03-MAR-2005.
XX
PF   31-OCT-2003; 2003US-00698907.
XX
PR   09-NOV-2001; 2001US-0345206P.
PR   02-JUL-2002; 2002US-03932772P.
PR   08-NOV-2002; 2002US-00291290.
PR   03-APR-2003; 2003US-0460488P.
XX
PT   Use of ephrin and its molecules for alleviating a symptom or a disorder
PT   with reduced levels of hematopoiesis, increased levels of cellular
PT   proliferation in an intestinal tract, or abnormal level of cellular
PT   proliferation in a tissue.
XX
CC   The invention relates to a novel use of ephrin, ephrin inhibitors, and
CC   ephrin receptors for alleviating a symptom of a disorder having reduced
CC   levels of hematopoiesis, having increased levels of cellular
CC   proliferation in an intestinal tract, or having an abnormal level of
CC   cellular proliferation in a tissue. A composition of the invention has
CC   cytostatic, antianemic, antiinflammatory, antipsoriatic, gastrointestinal
CC   -gen., dermatological, coagulant, immunostimulant, cerebroprotective,
CC   vasotropic, and antiulcer activity. The present sequence represents
CC   murine ephrin-B2.
XX
PS   Disclosure; SEQ ID NO 7; 68pp; English.
XX
SQ   Sequence 336 AA;

Query Match   45.7%; Score 628.5; DB 9; Length 336;
Best Local Similarity   41.8%; Pred. No. 3.8e-44;
Matches 137; Conservative   49; Mismatches 129; Indels 13; Gaps   5;

Qy   14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVYLYPQIGDRLDLLCPRARPPGPHSS   73
              |::| |||||| :||||||||:||||:|||:|||||:|||:||||| ::
Db   17 GLIMVLCRTAISRSIVLEPIYWNSSNSKFLPGGLVLYPQIGDKLDIICPKV---DSKTV   73

Qy   74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
              |:| |||| |||||:| :||||| ||:| ||:|||||||:||||||||||:||||
Db   74 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQQNK 133

Qy   134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPER-DR 190
              ||||:| ::||| |||||:||||||||||||| |||||||:|||:||| ||
Db   134 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

Qy   191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
              |:||||| |||||| |||||:|:| |||| : ||:||:||| ||||||||||||:
Db   194 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVLLL 253

Qy   251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
              ||| ::
Db   194 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVLLL 253

RESULT 15
ID   ADYS1238 standard; protein; 336 AA.
XX
AC   ADYS1238;
XX
ID   ADYS1238

```
Db   254  KYRRHRKHSPQHTTTLSLSTLLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH 306

Qy   311  YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
          ||||||||||||||||: |||| ||||
Db   307  YEKVSGDYGHPVYIVQEMPPQSPANIYY 334
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Search completed: December 21, 2005, 14:30:18
Job time : 156.239 secs

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OM protein - protein search, using sw model

Run on: December 21, 2005, 14:17:53 ; Search time 113.761 Seconds
                                                Copyright (c) 1993 - 2005 Compugen Ltd.
                                                GenCore version 5.1.6
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Title: US-10-021-121-4
Perfect score: 1850
Sequence: 1 MGPPHSGPGGVRGALLLLG...........PVYIVQDGPPQSPPNIYYKV 340

Scoring table: BLOSUM62
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Searched: 2443163 seqs, 43978781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   A_Geneseq_21:*
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               6: geneseqp2003aa:*
               7: geneseqp2003bs:*
               8: geneseqp2004s:*
               9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length Match	DB	ID	Description
1	1850	100.0	340	2	AAW31544	Human cyt
2	1850	100.0	340	2	AAW33699	AL-2-shor
3	1850	100.0	340	2	AAW10637	NLRRK2 li
4	1850	100.0	340	6	ABU07845	Human eph
5	1850	100.0	340	8	ADQ21436	Human sof
6	1850	100.0	340	9	ADY51247	Human eph
7	1844	99.7	340	2	AAW17081	EPH famil
8	1841	99.5	455	2	AAW33698	AL-2-long
9	1836	99.2	340	2	AAW46615	Human tra
10	1780	96.2	340	6	ABU07846	Mouse eph
11	1780	96.2	340	9	ADY51239	Mouse eph
12	1559	84.3	285	7	ADJ70889	Human hea
13	637.5	34.5	334	2	AAW00287	Mouse Eph
14	637.5	34.5	336	2	AAR92742	Murine he
15	635.5	34.4	336	6	ABU07844	Mouse eph
16	635.5	34.4	336	9	ADY51238	Mouse eph
17	632	34.2	346	2	AAR55059	Elk tyros
18	632	34.2	346	2	AAR91930	Human cyt
19	632	34.2	346	2	AAW19249	Human elk
20	632	34.2	346	2	AAW36055	Human elk
21	632	34.2	346	2	AAW44323	Human elk
22	632	34.2	346	6	ABU07841	Human eph
23	632	34.2	346	7	ABU62401	Human elk
24	632	34.2	346	7	ADN95630	Human BEC
25	632	34.2	346	8	ADH76244	Human nov
26	632	34.2	346	8	ADO28631	Human Epr
27	632	34.2	346	8	ADR73462	Human eph
28	632	34.2	346	6	ADV97175	Human eph
29	632	34.2	346	9	ADY51245	Human eph
30	631	34.1	346	2	AAR82606	Eph trans
31	630.5	34.1	331	2	AAW00288	Chicken E
32	629.5	34.0	331	2	AAR94655	Ligand fo
33	629.5	34.0	333	2	AAR92743	Human hep
34	629.5	34.0	333	2	AAR82287	Human LER
35	629.5	34.0	333	2	AAW06337	Full leng
36	629.5	34.0	333	2	AAW11308	Receptor-
37	629.5	34.0	333	6	ABU07886	Novel hum
38	629.5	34.0	333	7	ADD89059	TAT245. 1
39	629.5	34.0	333	8	ADN03886	Antipsori
40	629.5	34.0	333	8	ADP26886	Human Eph
41	629.5	34.0	333	8	ADR67298	Human bla
42	629.5	34.0	333	8	ADR86706	Human Eph
43	629.5	34.0	333	8	ADR82653	Human Eph
44	629.5	34.0	333	9	ADV73221	Human col
45	629.5	34.0	333	9	ADY51246	Human eph

ALIGNMENTS

RESULT 1
AAW31544

ID   AAW31544 standard; protein; 340 AA.
AC   AAW31544;
DT   14-APR-1998 (first entry)
DE   Human cytokine Lerk-8.
KW   Lerk-8; cytokine; human; hek; elk; receptor tyrosine kinase; ligand;
KW   neurodegenerative disease; wound healing; neovascularisation; diagnosis;
KW   therapy.
OS   Homo sapiens.
FH   Key   Location/Qualifiers
FH
FT   Peptide   1..27
FT   /label= Sig_peptide
FT   Protein   28..340
FT   /label= Mat_protein
FT   Domain   28..224
FT   /note= "extracellular domain"
FT   Modified-site   210..212
FT   /note= "N-glycosylated"
FT   Domain   225..251
FT   /note= "transmembrane domain"
FT   Domain   252..340
FT   /note= "cytoplasmic domain"
FT   Misc-difference 325
FT   /note= "residue 325 is Leu in Lerk-8 variant"
XX
PN   WO9736919-A2.
XX
PD   09-OCT-1997.
XX
PF   19-MAR-1997; 97WO-US004533.
XX
PR   21-MAR-1996; 96US-00621146.
XX
PA   (IMMV) IMMUNEX CORP.
XX
PI   Cerretti DP;
XX
DR   WPI; 1997-503043/46.
DR   N-PSDB; AAT89519.

PT   New isolated cytokine, Lerk-8 - binds to the hek and elk receptor
PT   tyrosine kinases, used to develop products for diagnosis and therapy.
XX
PS   Claim 3; Page 32-33; 37pp; English.
XX
CC   This protein sequence comprises a novel human cytokine designated Lerk-8.
CC   The amino acid sequence was deduced from a human foetal brain cDNA clone
CC   (see AAT89519). Lerk-8 binds to the cell surface receptors hek and elk,
CC   which are members of the eph/elk family of receptor tyrosine kinases.
CC   Lerk-8 polypeptides, especially soluble polypeptides comprising amino
CC   acid residues -27 to 142-197 of the full-length protein, can be expressed
CC   in transformed host cells. These polypeptides can be used to purify hek
CC   or elk proteins, and to purify or identify cells that express hek or elk
CC   on the surface. Such cells can be used in various in vitro studies or in
CC   vivo procedures, e.g. neural cells expressing elk can be administered to
CC   a mammal afflicted with a neurodegenerative disorder. The Lerk-8
CC   polypeptides can also be used to deliver diagnostic or therapeutic agents
CC   to thee cells (e.g. leukaemia cells). The Lerk-8 DNA and polypeptides
CC   can also be used to: treat disorders mediated by defective or
CC   insufficient amounts of Lerk-8; to treat disorders such as injury to
CC   neural tissue or neurologic disease; to promote angiogenesis; and for
CC   wound healing or stimulating neovascularisation of grafted tissues
XX
SQ   Sequence 340 AA;

Query Match   100.0%; Score 1850; DB 2; Length 340;
Best Local Similarity   100.0%;
Matches 340; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MGPPHSGPGGVRVGALILLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGPPHSGPGGVRVGALILLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy   61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLLTRGMKVLLRVGQSPRGGAVPRKP 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy   181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy   241 GVAGAGGAMCWRRRARKPSESRHPGGSFGRGGSLGLGGGGGWGPREAEPGELGIALRGG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GVAGAGGAMCWRRRARKPSESRHPGGSFGRGGSLGLGGGGGWGPREAEPGELGIALRGG 300

Qy   301 GAADPPFPCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYXKV 340
           ||||||||||||||||||||||||||||||||||||||||
Db   301 GAADPPFPCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYXKV 340

RESULT 2
ID   AAW33699
AC   AAW33699;

DT   30-APR-1998 (first entry)
XX
DE   AL-2-short (AL-2s) protein.
XX
OS   Homo sapiens.
XX
KW   AL-2s; AL-2; AL-2-short; human; treatment; neurological disorder; tumour;
KW   rheumatoid arthritis; wound healing; paralysis; angiogenesis; leukaemia;
KW   psoriasis; Alzheimer's disease; epilepsy.
XX
FH   Key   Location/Qualifiers
FT   Peptide   1..26
FT   /note= "signal peptide"
FT   Protein   27..340
FT   /note= "mature protein"
FT   Domain   27..219
FT   /note= "extracellular domain"
FT   Domain   220..245
FT   /note= "hydrophobic transmembrane domain"
XX
PN   WO9740153-A1.
XX
PD   30-OCT-1997.
XX
PF   17-APR-1997; 97WO-US006345.
XX
PR   19-APR-1996; 96US-00635130.
XX
PA   (GETH) GENENTECH INC.
XX
PI   Caras IW;
XX
DR   WPI; 1997-535837/49.
DR   N-PSDB; AAV06355.
XX
PT   Human AL-2 neurotrophic factor and related DNA - used to develop products
PT   for, e.g. treating neurologic disorders, angiogenesis disorders, tumours
PT   or rheumatoid arthritis or for wound healing.
XX
PS   Claim 20; Fig 2A-B; 86pp; English.
XX
CC   This is a AL-2-short (AL-2s) protein. The AL-2 is a novel Eph-related
CC   tyrosine kinase receptor ligand. AL-2 can be administered to patients in
CC   whom the nervous system has been damaged by trauma, surgery, stroke,
CC   ischaemia, infection, metabolic disease, nutritional deficiency,
CC   malignancy, or toxic agents, to promote the survival or growth of
CC   neurons. They can be used to treat motoneuron disorders such as
CC   amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, and
CC   various conditions involving spinal muscular atrophy, or paralysis. AL-2
CC   can be used to treat human neurodegenerative disorders, such as
CC   Alzheimer's disease, Parkinson's disease, epilepsy, demyelinating
CC   diseases such as multiple sclerosis, Huntingtons chorea, Down's syndrome,
CC   nerve deafness, Meniere's disease, and other disorders of the cerebellum.
CC   AL-2 can be used as cognitive enhancer, to enhance learning particularly
CC   in dementias or trauma, since they can promote axonal outgrowth and
CC   synaptic plasticity, particularly of hippocampal neurons that express AL-
CC   2 binding Eph-family receptors and cortical neurons that express AL-2. AL
CC   -2 can also be used for wound healing, i.e. accelerating
CC   neovascularisation of, e.g. burns and ulcers. The encoding nucleic acids
CC   are useful in preparing antibodies that specifically bind to the AL-2
CC   protein. The antibodies and the AL-2 antagonists are useful in diagnosing
CC   and treating various neuronal disorders. AL-2 antagonists can be used for
CC   modulating angiogenesis. They can also be used for the treatment of
CC   tumours, acute myeloid leukaemia (AML), chronic myeloid leukaemia (CML),
CC   myelodysplastic syndrome (MDS), diabetic retinopathy, neovascular
CC   glaucoma, psoriasis and rheumatoid arthritis
XX
SQ   Sequence 340 AA;

Query Match   100.0%; Score 1850; DB 2; Length 340;
Best Local Similarity   100.0%;
Matches 340; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MGPPHSGPGGVRVGALILLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGPPHSGPGGVRVGALILLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy   61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLLTRGMKVLLRVGQSPRGGAVPRKP 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy   181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

```
Db
Qy  181 VSEMPMERDRGAAHSLEPGKENLPGDPPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GVAGAGGAMCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG 300
Qy  241 GVAGAGGAMCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  301 GAADPPPCPHYEKVSGDYGHPVYIVQDGPPQSSPPNIYYKV 340
Qy  301 GAADPPPCPHYEKVSGDYGHPVYIVQDGPPQSSPPNIYYKV 340
        |||||||||||||||||||||||||||||||||||||||||
Db  301 GAADPPPCPHYEKVSGDYGHPVYIVQDGPPQSSPPNIYYKV 340
```

RESULT 3
ID   AAW10637 standard; protein; 340 AA.
XX
AC   AAW10637;
XX
DT   23-JUN-1997 (first entry)
XX
DE   NLERK2 ligand for eph-related kinase.
XX
KW   LERK; ligand for eph-related kinase; ERK; NLERK2;
KW   receptor protein tyrosine kinase; cell proliferation;
KW   cell differentiation; cell survival; nerve cell.
XX
OS   Homo sapiens.
XX
FH   Key   Location/Qualifiers
FH
FT   Peptide   1..29
FT   /label= Sig_peptide
FT   Protein   30..340
FT   /label= Mat_protein
FT   Modified-site   210
FT   /label= N-glycosylation_site
FT   Domain   227..251
FT   /label= Transmembrane_domain
XX
PN   WO9704091-A1.
XX
PD   06-FEB-1997.
XX
PF   19-JUL-1996; 96WO-AU000460.
PR   20-JUL-1995; 95AU-00004263.
PR   27-NOV-1995; 95AU-00006847.
PR   22-DEC-1995; 95AU-00007299.
PR   05-FEB-1996; 96AU-0007890.
XX
PA   (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI   Nicola NA;
XX
DR   WPI; 1997-132632/12.
DR   N-PSDB; AAT60966.
XX
PT   Nucleic acid mol. encoding ligand for eph-related kinase - useful for
PT   treatment of, pref. neuronal, cells to increase survival, proliferation
PT   and differentiation.
XX
PS   Claim 16; Page 37-39; 71pp; English.
XX
CC   A novel human ligand for eph-related kinase (LERK) is designated NLERK2
CC   (AAW10637). It is encoded by a cDNA clone (AAT60966) obtd. from a human
CC   foetal brain cDNA library. The novel receptor ligand can be expressed in
CC   transformed host cells and used in methods for regulating the
CC   development, maintenance or regeneration of different cells (e.g.
CC   neurons) and tissues in vivo and in vitro. Soluble NLERK2 peptides can be
CC   used to treat injury, disease or abnormality in the nervous system, and
CC   membrane-bound NLERK2 to modulate proliferation, different or survival
CC   e.g. in grafting procedures or transplantation. NLERK2 can also be used
CC   to raise antibodies for use in immunotherapy, and to detect anti-NLERK2
CC   antibodies that may occur in some autoimmune diseases

XX
SQ   Sequence 340 AA;
XX
```
Query Match             100.0%;  Score 1850;  DB 2;  Length 340;
Best Local Similarity   100.0%;  Pred. No. 2.5e-142;
Matches  340;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1 MGPPHSGPGGVRVGALLLLGVLGLVSGLLSLEPVYWNSANKRFQAEGGYYLYPQIGDRLDL 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MGPPHSGPGGVRVGALLLLGVLGLVSGLLSLEPVYWNSANKRFQAEGGYYLYPQIGDRLDL 60

Qy   61 LCPPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LCPPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy  121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy  181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy  241 GVAGAGGAMCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GVAGAGGAMCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG 300

Qy  301 GAADPPPCPHYEKVSGDYGHPVYIVQDGPPQSSPPNIYYKV 340
        |||||||||||||||||||||||||||||||||||||||||
Db  301 GAADPPPCPHYEKVSGDYGHPVYIVQDGPPQSSPPNIYYKV 340
```

RESULT 4
ID   ABU07845 standard; protein; 340 AA.
XX
AC   ABU07845;
XX
DT   10-MAY-2003 (first entry)
XX
DE   Human ephrin-B3 ligand.
XX
KW   Cytostatic; vasodilator; antiinflammatory; cardiant; gene therapy;
KW   ligand-receptor binding modulator; ephrin ligand; angiogenesis;
KW   lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;
KW   cell migration disorder; cell proliferation disorder; neovascularisation;
KW   ischaemia; infarction; tissue graft; transplant; human; ephrin-B3;
KW   tie receptor tyrosine kinase; Eph receptor ligand.
XX
OS   Homo sapiens.
XX
PN   WO2003004529-A2.
XX
PD   16-JAN-2003.
XX
PF   02-JUL-2002; 2002WO-IB002524.
XX
PR   02-JUL-2001; 2001US-0302960P.
XX
PA   (LICN) LICENTIA LTD.
XX
PI   Alitalo K, Kubo Hi;
XX
DR   WPI; 2003-210341/20.
DR   N-PSDB; ABX12546.
XX
PT   Identifying modulators of binding between a Tie receptor tyrosine kinase
PT   and an Ephrin ligand, useful for promoting neovascularization, comprises
PT   contacting a Tie receptor with an Ephrin in the presence of a putative
PT   modulator.
XX
PS   Disclosure; Page 117-119; 199pp; English.
XX

CC The invention describes a method of identifying a modulator of binding
CC between a Tie receptor tyrosine kinase and an Ephrin ligand. The method
CC comprises contacting a Tie receptor composition with an Ephrin
CC composition in the presence and in the absence of a putative modulator
CC compound, and detecting the binding between the Tie receptor and the Ephrin
CC compound, and detecting the binding between the Tie receptor and the Ephrin
CC in the presence and in the absence of the putative modulator. The method
CC is useful for identifying a modulator of binding between a Tie receptor
CC tyrosine kinase and an Ephrin ligand. Modulators identified from the
CC method are useful in modulating angiogenic processes, including
CC lymphangiogenesis, for treating diseases associated with aberrant Ephrin-
CC Tie biology, aberrant growth, migration or proliferation of cells that
CC express a Tie receptor, or for promoting growth of vessel or
CC neovascularisation (e.g. ischaemic tissue, an infarction, a new or
CC chronic compound, or a tissue graft or transplant). This is the amino
CC acid sequence of human Ephrin-B3, a member of the Ephrin-B subclass of
CC ligands that are bound to the membrane via a transmembrane domain and
CC short cytoplasmic tail and function as Eph receptor ligands
XX
SQ Sequence 340 AA;

Query Match   100.0%; Score 1850; DB 6; Length 340;
Best Local Similarity   100.0%;
Matches 340; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MGPPHSGPGGVRVGALLLLGVLLGLVSGLLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGPPHSGPGGVRVGALLLLGVLLGLVSGLLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy   61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy   181 VSEMPMERDRGAAHSLEPGKENLPGDPTPSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 VSEMPMERDRGAAHSLEPGKENLPGDPTPSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy   241 GVAGAGGAMCWRRRAKPSESRHPGPGSFGRGGSSLGLGGGGGMGPREAEPGELGIALRGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GVAGAGGAMCWRRRAKPSESRHPGPGSFGRGGSSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy   301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
              ||||||||||||||||||||||||||||||||||||||||
Db   301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340

RESULT 5
ID   ADQ21436
AC   ADQ21436;
XX
DT   26-AUG-2004 (first entry)
XX
DE   Human soft tissue sarcoma-upregulated protein - SEQ ID 4256.
XX
KW   soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
XX
OS   Homo sapiens.
XX
PN   WO200048938-A2.
XX
PD   10-JUN-2004.
XX
PF   26-NOV-2003; 2003WO-US038193.
XX
PR   26-NOV-2002; 2002US-0429739P.
XX
PA   (PROT-) PROTEIN DESIGN LABS INC.
XX
,XX

PI   Aziz N, Ginsburg WM, Zlotnik A;
XX
DR   WPI; 2004-441208/41.

PT   Early detection of soft tissue sarcoma comprises determining expression
PT   of a gene in a first soft tissue sample and a normal soft tissue sample
PT   and comparing the gene expression, also useful in treating soft tissue
PT   sarcoma.
XX
PS   Example 2; SEQ ID NO 4256; 210pp; English.
XX
CC The invention relates to a novel method for detecting soft tissue sarcoma
CC which comprises obtaining a first soft tissue sample from an individual
CC and a normal soft tissue sample from the same or different individual,
CC determining the expression of a gene in both samples and comparing the
CC expression of the gene in the first soft tissue samples, where a higher level
CC of protein expression in the first soft tissue sample indicates the
CC presence of soft tissue sarcoma. The method of the invention has
CC cytostatic applications and may be useful for detecting soft tissue
CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
CC acid sequences may be useful in diagnostic and screening applications.
CC The current sequence is that of a human soft tissue sarcoma-upregulated
CC protein of the invention. The current sequence is not shown within the
CC specification per se but was submitted in CD format by the inventor.
XX
SQ Sequence 340 AA;

Query Match   100.0%; Score 1850; DB 8; Length 340;
Best Local Similarity   100.0%;
Matches 340; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MGPPHSGPGGVRVGALLLLGVLLGLVSGLLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGPPHSGPGGVRVGALLLLGVLLGLVSGLLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy   61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy   181 VSEMPMERDRGAAHSLEPGKENLPGDPTPSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 VSEMPMERDRGAAHSLEPGKENLPGDPTPSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy   241 GVAGAGGAMCWRRRAKPSESRHPGPGSFGRGGSSLGLGGGGGMGPREAEPGELGIALRGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GVAGAGGAMCWRRRAKPSESRHPGPGSFGRGGSSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy   301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
              ||||||||||||||||||||||||||||||||||||||||
Db   301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340

RESULT 6
ID   ADY51247
AC   ADY51247;
XX
DT   19-MAY-2005 (first entry)
XX
DE   Human ephrin-B3 SEQ ID NO:16.
XX
KW   ephrin; hematopoiesis; hyperproliferation; cytostatic; antianemic;
KW   antiinflammatory; antipsoriatic; gastrointestinal-gen.; dermatological;
KW   coagulant; immunostimulant; cerebroprotective; vasotropic; antiulcer.
XX
OS   Homo sapiens.
XX
PN   US2005049194-A1.

Left column:

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XX
PD   03-MAR-2005.
XX
PF   31-OCT-2003; 2003US-00698907.
XX
PR   09-NOV-2001; 2001US-03452206P.
PR   02-JUL-2002; 2002US-0393272P.
PR   08-NOV-2002; 2002US-00291290.
PR   03-APR-2003; 2003US-0460488P.
XX
XX
PA   (FRIS/) FRISEN J.
PA   (HOLM/) HOLMBERG J.
XX
PI   Frisen J, Holmberg J;
XX
DR   WPI; 2005-195317/20.
XX
PS   Disclosure; SEQ ID NO 16; 68pp; English.
XX
PT   Use of ephrin and its molecules for alleviating a symptom or a disorder
PT   with reduced levels of hematopoiesis, increased levels of cellular
PT   proliferation in an intestinal tract, or abnormal level of cellular
PT   proliferation in a tissue.
XX
CC   The invention relates to a novel use of ephrin, ephrin inhibitors, and
CC   ephrin receptors for alleviating a symptom of a disorder having reduced
CC   levels of hematopoiesis, having increased levels of cellular
CC   proliferation in an intestinal tract, or having an abnormal level of
CC   cellular proliferation in a tissue. A composition of the invention has
CC   cytostatic, antianemic, antiinflammatory, antipsoriatic, gastrointestinal
CC   -gen., dermatological, coagulant, immunostimulant, cerebroprotective,
CC   vasotropic, and antiulcer activity. The present sequence represents
CC   murine ephrin-B3.
XX
SQ   Sequence 340 AA;

Query Match             100.0%;  Score 1850;  DB 9;  Length 340;
Best Local Similarity   100.0%;
Matches  340;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy        1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy       61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy      121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy      181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL 240

Qy      241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy      301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSSPNIYYKV 340
            ||||||||||||||||||||||||||||||||||||||||
Db      301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSSPNIYYKV 340

RESULT 7
XX
AC   AAW17081;
XX
ID   AAW17081 standard; protein; 340 AA.
XX
AC   AAW17081;
XX
DT   09-AUG-1997  (first entry)
XX
```

Right column:

```
DE   EPH family ligand Efl-6.
XX
KW   Efl-6; Eph; Elk; receptor tyrosine kinase; signal transduction; ligand;
KW   neurological disease.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..24
FT                   /label= Sig_peptide
FT   Protein         25..340
FT                   /label= Mat_protein
FT   Misc-difference 166
FT                   /label= Gln, Arg
FT   Domain          225..249
FT                   /label= Transmembrane_domain
XX
PN   WO9715667-A1.
XX
PR   25-OCT-1995;  95US-00070015P.
XX
PD   01-MAY-1997.
XX
PF   25-OCT-1996;  96WO-US017201.
XX
PA   (REGE-) REGENERON PHARM INC.
XX
PI   Davis S, Gale NW, Yancopoulos GD;
XX
DR   WPI; 1997-259021/23.
DR   N-PSDB; AAT69808.
XX
PS   Claim 2; Fig 1; 36pp; English.
XX
PT   New nucleic acid encoding Efl-6 ligand protein - used for promoting
PT   growth and proliferation of neuronal cells and in drug screening.
XX
CC   A novel ligand (AAW17081), designated Efl-6 (or Eph transmembrane
CC   tyrosine kinase family ligand 6), binds to the Elk, Nuk/Cek5, Hek2/Sek4,
CC   Htk and Sek1 receptors on cells. Its amino acid sequence was deduced from
CC   a human frontal cortex cDNA clone (AAT69808). Recombinant Elf-6,
CC   truncated soluble polypeptides comprising the extracellular domain of Elf
CC   -6, and Efl-6 ligandbodies comprising soluble Efl-6 and the Fc portion of
CC   IgG can be expressed in host cells. These can be used to support neuronal
CC   and other Eph receptor-bearing cell populations for treatment of
CC   neurological disorders, in drug screening and to raise diagnostic
CC   antibodies
XX
SQ   Sequence 340 AA;

Query Match              99.7%;  Score 1844;  DB 2;  Length 340;
Best Local Similarity    99.7%;
Matches  339;  Conservative   0;  Mismatches   1;  Indels   0;  Gaps   0;

Qy        1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy       61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy      121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLXVGQSPRGGAVPRKP 180
            ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db      121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy      181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL 240

Qy      241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
```

```
Qy    301 GAADPPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYXKV 340
          |||||||||||||||||||||||||||||||||||||||||
Db    301 GAADPPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYYKV 340

RESULT 8
ID   AAW33698
AAW33698 standard; protein; 455 AA.
XX
AC   AAW33698;
XX
DT   30-APR-1998  (first entry)
XX
DE   AL-2-long (AL-21) protein.
XX
KW   AL-21; AL-2; AL-2-long; human; treatment; neurological disorder; tumour;
KW   rheumatoid arthritis; wound healing; paralysis; angiogenesis; leukaemia;
KW   psoriasis; Alzheimer's disease; epilepsy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..26
FT                   /note= "signal peptide"
FT   Protein         27..455
FT                   /note= "mature protein"
FT   Domain          27..219
FT                   /note= "extracellular domain"
FT   Domain          220..245
FT                   /note= "hydrophobic transmembrane domain"
XX
PN   WO9740153-A1.
XX
PD   30-OCT-1997.
XX
PF   17-APR-1997;  97WO-US006345.
PR   19-APR-1996;  96US-0063513O.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Caras IW;
XX
DR   WPI; 1997-535837/49.
DR   N-PSDB; AAV06354.
XX
PT   Human AL-2 neurotrophic factor and related DNA - used to develop products
PT   for, e.g. treating neurologic disorders, angiogenesis disorders, tumours
PT   or rheumatoid arthritis or for wound healing.
XX
PS   Claim 20; Fig 1A-C; 86pp; English.
XX
CC   This is a AL-2-long (AL-21) protein. The AL-2 is a novel Eph-related
CC   tyrosine kinase receptor ligand. AL-2 can be administered to patients in
CC   whom the nervous system has been damaged by trauma, surgery, stroke,
CC   ischaemia, infection, metabolic disease, nutritional deficiency,
CC   malignancy, or toxic agents; to promote the survival or growth of
CC   neurons. They can be used to treat motoneuron disorders such as
CC   amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, and
CC   various conditions involving spinal muscular atrophy, or paralysis. AL-2
CC   can be used to treat human neurodegenerative disorders, such as
CC   Alzheimer's disease, Parkinson's disease, epilepsy, demyelinating
CC   diseases such as multiple sclerosis, Huntington's chorea, Down's syndrome,
CC   nerve deafness, Menier's disease, and other disorders of the cerebellum.
CC   AL-2 can be used as cognitive enhancer, to enhance learning particularly
CC   in dementias or trauma, since they can promote axonal outgrowth and
CC   synaptic plasticity, particularly of hippocampal neurons that express AL-
CC   2 binding Eph-family receptors and cortical neurons that express AL-2. Al
CC   -2 can also be used for wound healing, i.e. accelerating
CC   neovascularisation of, e.g. burns and ulcers. The encoding nucleic acids
CC   are useful in preparing antibodies that specifically bind to the AL-2
CC   protein. The antibodies and the AL-2 antagonists are useful in diagnosing
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CC   and treating various neuronal disorders. AL-2 antagonists can be used for
CC   modulating angiogenesis. They can also be used for the treatment of
CC   tumours, acute myeloid leukaemia (AML), chronic myeloid leukaemia (CML),
CC   myelodysplastic syndrome (MDS); diabetic retinopathy, neovascular
CC   glaucoma, psoriasis and rheumatoid arthritis
XX
SQ   Sequence 455 AA;

Query Match             99.5%;  Score 1841; DB 2; Length 455;
Best Local Similarity   100.0%;  Pred. No. 1.9e-141;
Matches  338;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPYVWNSANKRFQAEGGYVLYPQIGDRLDL 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPYVWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy     61 LCPRARPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LCPRARPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy    121 SPNLWGHEFRSHHDYYIIATSDGTREGLLESLQGGVCLTRGMKVLLLRVGQSPRGGAVPRKP 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SPNLWGHEFRSHHDYYIIATSDGTREGLLESLQGGVCLTRGMKVLLLRVGQSPRGGAVPRKP 180

Qy    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL 240

Qy    241 GVAGAGGAMCWRRRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GVAGAGGAMCWRRRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG 300

Qy    301 GAADPPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYY 338
          |||||||||||||||||||||||||||||||||||||||
Db    301 GAADPPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYY 338

RESULT 9
ID   AAW46615
AAW46615 standard; protein; 340 AA.
XX
AC   AAW46615;
XX
DT   06-JUL-1998  (first entry)
XX
DE   Human transmembrane ligand Elk-L3.
XX
KW   Elk-L3; Elk-related receptor tyrosine kinase; transmembrane ligand;
KW   human; signal transduction; axonogenesis; nerve cell; neurone;
KW   Alzheimer's disease; Parkinson's disease; Huntingdon's disease;
KW   demyelination; multiple sclerosis; amyotrophic lateral sclerosis;
KW   nervous system infection; Wernicke's disease; trauma; ischaemia; stroke;
KW   nutritional polyneuropathy; progressive supranuclear palsy;
KW   Shy Drager's syndrome; multistem degeneration;
KW   olivo ponto cerebellar atrophy, peripheral nerve damage.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 166
FT                   /label= Gln, Arg
FT   Domain          225..249
FT                   /note= "transmembrane domain"
XX
PN   WO9801548-A1.
XX
PD   15-JAN-1998.
XX
PF   04-JUL-1997;  97WO-CA000473.
PR   05-JUL-1996;  96US-0021272P.
XX
PA   (MOUN ) MOUNT SINAI HOSPITAL CORP.
```

```
AC   ABU07846;
XX
ID   ABU07846 standard; protein; 340 AA.
ABU07846
RESULT 10

Db   301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPQNIYYKV 340
            |||||||||||||||||||||||||||||||||||||||
Qy   301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPQNIYYKV 340

Db   241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFCRGGSLGLGGGGGMGPRBAEPGELGIALRGG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFCRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Db   181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Db   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Db    61 LCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLTCDRPDLDLRFTIKFQEY 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    61 LCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLTCDRPDLDLRFTIKFQEY 120

Db     1 MGPPHSGPGGGVRVGALLLLGVILGVLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy     1 MGPPHSGPGGGVRVGALLLLGVILGVLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Matches 338; Conservative   0; Mismatches   2; Indels   0; Gaps   0;
Best Local Similarity   99.4%;   Pred. No. 3.5e-141;
Query Match   99.2%;   Score 1836;   DB 2;   Length 340;

Sequence 340 AA;
SQ
XX
CC   stroke.
CC   atrophy, peripheral nerve damage, trauma, and ischaemia resulting from
CC   Drager's syndrome, multisystem degeneration and olivo ponto cerebellar
CC   and nutritional polyneuropathy, progressive supranuclear palsy, Shy
CC   of the nervous system deficiency diseases, such as Wernicke's disease
CC   sclerosis, amyotrophic lateral sclerosis, bacterial and viral infections
CC   disease, Huntingdon's disease, demyelinating diseases, such as multiple
CC   injury to the nervous system, such as Alzheimer's disease, Parkinson's
CC   regeneration, to treat diseases and conditions involving trauma and
CC   be used to modulate axonogenesis, nerve cell interactions and
CC   in a subject (all claimed). The substances identified by the methods can
CC   regeneration in a subject, or in a medicament for modulating axonogenesis
CC   preparation of a medicament for modulating neuronal development or
CC   ERRTK. A purified and isolated oligomerised ERRTK can be used in the
CC   identify substances that affect or modulate a pathway regulated by a
CC   the biological activity of a transmembrane ligand for an ERRTK, and to
CC   can also be used for evaluating a substance for its ability to modulate
CC   ERRTK, and the transmembrane ligand expressed on the cell. The complex
CC   oligomerised ERRTK, or an isoform or an extracellular domain of the
CC   transmembrane ligand comprises forming a complex between a purified and isolated
CC   the biological activity of, or for affecting a pathway regulated by, a
CC   related receptor tyrosine kinase (ERRTK). A novel method of modulating
CC   This polypeptide comprises human Elk-L3, a transmembrane ligand of Elk-
XX
PS   Disclosure; Fig 5A; 40pp; English.
XX
PT   receptor tyrosine kinase and a transmembrane ligand.
PT   kinase - by formation of a complex between an oligomerised Elk-related
PT   Modulating transmembrane ligand for an Elk-related receptor tyrosine
XX
DR   N-PSDB; AAV16097.
DR   WPI; 1998-101047/09.
XX
PI   Holland S, Mbamalu G, Pawson T;
XX
```

```
Qy   181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Db   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Db    61 LCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLTCDRPDLDLRFTIKFQEY 120
            |||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Qy    61 LCPRARPPGPHSSSYEFYKLYLVGGAQGRRCEAPPAPNLLTCDRPDLDLRFTIKFQEY 120

Db     1 MGAPHPGPGGGVQVGALLLJGPAGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
            || |||:||||| ||:||||||  ||||||||||||||||||||||||||||||||| ||
Qy     1 MGPPHSGPGGGVRVGALLLLGVILGVLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Matches 325; Conservative   7; Mismatches   8; Indels   0; Gaps   0;
Best Local Similarity   95.6%;   Pred. No. 1.3e-136;
Query Match   96.2%;   Score 1780;   DB 6;   Length 340;

Sequence 340 AA;
SQ
XX
CC   short cytoplasmic tail and function as Eph receptor ligands
CC   ligands that are bound to the membrane via a transmembrane domain and
CC   acid sequence of mouse Ephrin-B3, a member of the Ephrin-B subclass of
CC   chronic compound, or a tissue graft or transplant). This is the amino
CC   neovascularisation (e.g. ischaemic tissue, an infarction, a new or
CC   express a Tie receptor, or for promoting growth of vessel or
CC   Tie biology, aberrant growth, migration or proliferation of cells that
CC   lymphangiogenesis, for treating diseases associated with aberrant Ephrin-
CC   method are useful in modulating angiogenic processes, including
CC   tyrosine kinase and an Ephrin ligand. Modulators identified from the
CC   is useful for identifying a modulator of binding between a Tie receptor
CC   in the presence and in the absence of the putative modulator. The method
CC   compound, and detecting the binding between a Tie receptor and the Ephrin
CC   composition in the presence and in the absence of a putative modulator
CC   comprises contacting a Tie receptor composition with an Ephrin
CC   between a Tie receptor tyrosine kinase and an Ephrin ligand. The method
CC   The invention describes a method of identifying a modulator of binding
XX
PS   Disclosure; Page 121-122; 199pp; English.
XX
PT   modulator.
PT   contacting a Tie receptor with an Ephrin in the presence of a putative
PT   an Ephrin ligand, useful for promoting neovascularization, comprises
PT   Identifying modulators of binding between a Tie receptor tyrosine kinase
XX
DR   N-PSDB; ABX12547.
DR   WPI; 2003-210341/20.
XX
PN   WO2003004529-A2.
XX
OS   Mus musculus.
XX
DE   Mouse ephrin-B3 ligand.
XX
DT   10-MAY-2003 (first entry)
XX
```

```
Db           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   181   VSEMPMERDRGAAHSAEPGRDTIPGDPSSNATSRGAEGPLPPPSMPAVAGAAOGMALLL 240
           |::||||||||||||||||||||||||||||||||::|||||||||||||||||:|||||
Db

Qy   241   GVAGAGGAMCWRRRARAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db

Qy   301   GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
           |||||||||||||||||||||||||||||||||||||||
Db

Qy   301   GTADPPFCPHYEKVSGDYGHPVIIVQDGPPQSPPNIYYKV 340
           |||||||||||||||||||||||||||||||||||||||||

RESULT 11
ADY51239
ID   ADY51239 standard; protein; 340 AA.
XX
AC   ADY51239;
XX
DT   19-MAY-2005  (first entry)
XX
DE   Mouse ephrin-B3 SEQ ID NO:8.
XX
OS   Mus musculus.
XX
OC
XX
PN   US2005049194-A1.
XX
PD   03-MAR-2005.
XX
PF   31-OCT-2003; 2003US-00698907.
XX
PR   09-NOV-2001; 2001US-0345206P.
PR   02-JUL-2002; 2002US-0393272P.
PR   08-NOV-2002; 2002US-00291290.
PR   03-APR-2003; 2003US-0460488P.
XX
PT   Use of ephrin and its molecules for alleviating a symptom or a disorder
PT   with reduced levels of hematopoiesis, increased levels of cellular
PT   proliferation in an intestinal tract, or having an abnormal level of
PT   cellular proliferation in a tissue. A composition of the invention has
PT   cytostatic, antianemic, antiinflammatory, antipsoriatic, gastrointestinal
PT   -gen, dermatological, coagulant, immunostimulant, cerebroprotective,
PT   vasotropic, and antiulcer activity. The present sequence represents
PT   murine ephrin-B3.
XX
PS   Disclosure; SEQ ID NO 8; 68pp; English.
XX
CC   The invention relates to a novel use of ephrin, ephrin inhibitors, and
CC   ephrin receptors for alleviating a symptom of a disorder having reduced
CC   levels of hematopoiesis, having increased levels of cellular
CC   proliferation in an intestinal tract, or having an abnormal level of
CC   cellular proliferation in a tissue. A composition of the invention has
CC   cytostatic, antianemic, antiinflammatory, antipsoriatic, gastrointestinal
CC   -gen, dermatological, coagulant, immunostimulant, cerebroprotective,
CC   vasotropic, and antiulcer activity. The present sequence represents
CC   murine ephrin-B3.
XX
PA   (FRIS/) FRISEN J.
PA   (HOLM/) HOLMBERG J.
XX
PI   Frisen J, Holmberg J;
XX
DR   WPI; 2005-195317/20.
XX
PF   ephrin; hematopoiesis; hyperproliferation; cytostatic; antianemic;
KW   antiinflammatory; antipsoriatic; gastrointestinal-gen.; dermatological;
KW   coagulant; immunostimulant; cerebroprotective; vasotropic; antiulcer.
XX
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Qy    61   LCPRARPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61   LCPRARPGPHSSPSYEFYKLYLVEGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy   121   SPNIWGHEFRSHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGAQMALLL 180
           |||||||||:|||||||||||||||||||||||||||||||||||||||||||:|||||
Db   121   SPNIWGHEFRSHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGAVPRKP 180

Qy   181   VSEMPMERDRGAAHSAEPGRDTIPGDPTSNATSRGAEGPLPPPSMPAVAGAAOGMALLL 240
           ||||||||||||||||||||||||||::||||||||||||||||||||||||||:|||||
Db   181   VSEMPMERDRGAAHSAEPGRDTIPGDPSSNATSRGAEGPLPPPSMPAVAGAAOGMALLL 240

Qy   241   GVAGAGGAMCWRRRARAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241   GVAGAGGAMCWRRRARAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy   301   GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
           |||||||||||||||||||||||||||||||||||||||
Db   301   GTADPPFCPHYEKVSGDYGHPVIIVQDGPPQSPPNIYYKV 340

RESULT 12
AD770889
ID   AD770889 standard; protein; 285 AA.
XX
AC   AD770889;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Human heat mitochondrial protein as a therapeutic target SeqID2695.
XX
OS   Homo sapiens.
XX
OC
XX
PN   WO2003087768-A2.
XX
PD   23-OCT-2003.
XX
PF   04-APR-2003; 2003WO-US010870.
XX
PR   12-APR-2002; 2002US-0372843P.
PR   17-JUN-2002; 2002US-0389887P.
PR   20-SEP-2002; 2002US-0412418P.
XX
PT   Identifying a mitochondrial target for drug screening assays and for
PT   treating diseases associated with altered mitochondrial function,
PT   comprises detecting a modified polypeptide in a sample and correlating
PT   with the disease.
XX
PS   Claim 1; SEQ ID NO 2695; 180pp; English.
XX
CC   This invention relates to novel mitochondrial targets that can be used
CC   for therapeutic intervention in treating a disease associated with
CC   altered mitochondrial function. Specifically, it refers to a method for
CC   identifying proteins of the human heart mitochondrial proteome that are
CC   useful for drug screening assays, as well as therapeutic targets. The
CC   present invention describes a method for identifying such proteins that
CC   can be used in the treatment of various diseases associated with altered
```

```
PA   (MITO-) MITOKOR.
PA   (BUCK-) BUCK INST AGE RES.
XX
PI   Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM,
PI   Warnock DE;
XX
DR   WPI; 2003-845369/78.
XX
KW   mitochondrial; human; screening assay; diabetes mellitus;
KW   Huntington's disease; osteoarthritis;
KW   Leber's hereditary optic neuropathy; LHON;
KW   mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW   myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW   neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW   osteopathic; ophthalmological; cytostatic.
XX
```

```
SQ   Sequence 340 AA;
     Query Match             96.2%;  Score 1780; DB 9;  Length 340;
     Best Local Similarity   95.6%;  Pred. No. 1.3e-136;
     Matches  325;  Conservative   7;  Mismatches   8;  Indels    0;  Gaps    0;

Qy    1   MGPPHSGPGGVRVGALLLLGVLLGVLVSGLSLEPVYWNSANKRFQAEGGVYLYPQIGDRLDL 60
          ||| ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    1   MGAPHFGPGGVQVGALLLLGPAGLVSGLSLEPVYWNSANKRFQAEGGVYLYPQIGDRLDL 60
```

```
CC   mitochondrial function including diabetes mellitus, Huntington's disease,
CC   osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC   encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC   ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC   compositions have neuroprotective, nootropic, antidiabetic,
CC   anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC   cytostatic activities. This polypeptide sequence is a human heart
CC   mitochondrial protein of the invention.
XX
PS   Sequence 285 AA;
SQ

Query Match     84.3%;  Score 1559;  DB 7;  Length 285;
Best Local Similarity   100.0%;  Pred. No. 1.1e-118;
Matches  285;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     56 DRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQCRRCEAPPAAPNLLLTCDRPDLDLRFTI 115
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 DRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQCRRCEAPPAAPNLLLTCDRPDLDLRFTI 60

Qy    116 KFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLITRGMKVLLRVCQSPRGGA 175
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 KFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLITRGMKVLLRVCQSPRGGA 120

Qy    176 VPRKPVSEMPERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL 235
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 VPRKPVSEMPERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL 180

Qy    236 ALLLLGVAGAGGAMCWRRRRAKPSESRHPGPGSPGRGGSLGLGGGGMGPREAEPGELGI 295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 ALLLLGVAGAGGAMCWRRRRAKPSESRHPGPGSPGRGGSLGLGGGGMGPREAEPGELGI 240

Qy    296 ALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
          |||||||||||||||||||||||||||||||||||||||||||||
Db    241 ALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 285
```

```
RESULT 13
AAW00287
ID   AAW00287 standard; protein; 334 AA.
XX
AC   AAW00287;
XX
DT   19-JAN-1997  (first entry)
XX
DE   Mouse Eph receptor ligand ELF-2.
XX
KW   Eph receptor; ligand; ELF-2; tyrosine kinase; signal transduction;
KW   organogenesis; oncogenesis; tumour; neurological disorder; diagnosis;
KW   gene therapy.
XX
OS   Mus sp.
XX
FH   Key            Location/Qualifiers
FH
FT   Domain         1..224
FT                  /label= Extracellular_domain
FT   Binding-site   31..155
FT                  /label= Receptor_binding_site
FT   Domain         226..251
FT                  /label= Transmembrane_domain
XX
PN   WO9626958-A2.
XX
PD   06-SEP-1996.
XX
PF   23-FEB-1996; 96WO-US002673.
XX
PR   27-FEB-1995; 95US-00395415.
XX
PA   (HARD ) HARVARD COLLEGE.
XX
PI   Flanagan JG, Bergemann AD;
XX
DR   WPI; 1996-433391/43.
```

```
DR   N-PSDB; AAT40230.
XX
DE   Eph receptor ligand, ELF-2, and DNA encoding it ; used to treat or
PT   prevent neurological diseases, and to modulate binding of ELF-2 to Eph
PT   receptor, e.g. to prevent or treat tumour formation.
XX
CC   Claim 6; Fig 1A-B; 50pp; English.
XX
PS   Mouse Eph receptor ligand ELF-2 (AAW00287) is strongly expressed in the
CC   anterior hindbrain and newly-forming somites of embryos at the early
CC   organogenesis stage of development. Its amino acid sequence was
CC   communication during pattern formation. It is important in cellular
CC   deduced from a cDNA clone (AAT40230) isolated from a newborn mouse brain
CC   cDNA library. The ELF-2 ligand can be used to alter neurological
CC   development, oncogenesis and growth regulation, to modulate binding of
CC   ELF-2 to the Eph receptor, and in diagnostic assays
XX
SQ   Sequence 334 AA;

Query Match     34.5%;  Score 637.5;  DB 2;  Length 334;
Best Local Similarity   42.1%;  Pred. No. 1.8e-43;
Matches  139;  Conservative   49;  Mismatches  129;  Indels   13;  Gaps    5;

Qy     14 GALLILGVLGLVSGLSLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPGPHSS 73
          |:|:|      |||:|    :||  |||  :||:|  ||||:||||||||||||:||||
Db     15 GLIMVLCRTAISRSTVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 71

Qy     74 PNYEFYKLYLVGGAQCRRCEAPPAAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     72 GQYEYYKVXYMVDKDQADRCTTKKENTPLLNCARPDDDVKFTIKFQEFSPNLWGLEFQKNK 131

Qy    134 DYYIIATSDGTREGLESLQGGVCLITRGMKVLLRVCQ--SPRGGAVPRKPVSEMPMER-DR 190
          |:|  |   ||  |||:||||  |||   |||||||  :  ||: ||  |||:||: |
Db    132 DYYIISTSNGSLEGHLDNQEGGVCQTRAMKLIMKVSQDDASSAGSARNHGPTRPELEAGTN 191

Qy    191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
          |:|:  ||:   ||   ::: |||   |:|||||||:||: |||  |:||:||||:
Db    192 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLl 251

Qy    251 WRRRRAKPSESRHPGPGSPGRGGSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
          |||       ||||||||||||||  |||||||||:|||||||||||||||||||||
Db    252 KYRRHRHKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVPCPH 304

Qy    311 YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
          ||||||||||||||| ||||||||||||||
Db    305 YEKVSGDYGHPVYIVQEMPPQSPANIYYKV 334
```

```
RESULT 14
AAR92742
ID   AAR92742 standard; protein; 336 AA.
XX
AC   AAR92742;
XX
DT   21-MAY-1996  (first entry)
XX
DE   Murine hepatoma transmembrane kinase receptor ligand.
XX
KW   Hepatoma transmembrane kinase; Htk; receptor; ligand; tyrosine kinase;
KW   neurodegenerative disease.
XX
OS   Mus musculus.
XX
PN   WO9602645-A2.
XX
PD   01-FEB-1996.
XX
PF   14-JUL-1995; 95WO-US008812.
XX
PR   20-JUL-1994; 94US-00277722.
XX
PA   (GETH ) GENENTECH INC.
XX
```

```
PI   Bennett BD, Matthews W;
XX
DR   WPI; 1996-105907/11.
DR   N-PSDB; AAT16470.
XX
PT   Ligand for the hepatoma trans-membrane kinase receptor - useful for
PT   stimulating and inhibiting cells carrying the receptor, e.g. for treating
PT   neuro-degenerative disease.
XX
PS   Claim 5; Fig 1(A-D); 88pp; English.
XX
CC   Mouse (AAT16470) and human (AAT16471) Htk ligand which bind to, and
CC   activate, the Htk receptor, have been identified in a variety of tissues
CC   using a soluble Htk-Fc fusion protein. The predicted mol.wt. of the
CC   murine Htk ligand protein following a signal peptide cleavage is 34 kD
CC   with an estimated pI of 8.9. The murine and human ligands show 96%
CC   homology at the amino acid level. The DNA is used to produce recombinant
CC   ligands; for tissue- specific typing (partic. as a marker for breast
CC   cancer) and as a marker for human chromosome 13. The ligands (partic. in
CC   soluble form) are used to activate the tyrosine kinase domain of the Htk
CC   receptor, i.e. to stimulate or inhibit growth, differentiation, and/or
CC   activation of cells contg. the receptor, e.g. treatment of
CC   neurodegenerative diseases, since they are strongly expressed in the
CC   cerebral cortex, hippocampus, striatum and cerebellum. The ligands are
CC   also useful as a control or standard in assays, for generation of
CC   antibodies, as a mol. wt. marker, for growth in vitro of Htk-receptor
CC   positive cells, as research agent, in screening, etc
XX
SQ   Sequence 336 AA;

Query Match             34.5%;  Score 637.5;  DB 2;  Length 336;
Best Local Similarity   42.1%;  Pred. No. 1.8e-43;
Matches  139;  Conservative  49;  Mismatches  129;  Indels  13;  Gaps  5;

Qy           14 GALLLLGVLLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGHSS 73
                |::|   |||||||: ||:||: .||||||:||:|| :::||||||:||||::||:
Db           17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKIV 73

Qy           74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                |: |||:|   ||| ||||||||||||| |||||||||  ::||:|||:||||||
Db           74 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133

Qy          134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPER-DR 190
                |||| :|::|: |||:: :|||| : |  :|::.|||        .::    ::|: :
Db          134 DYYIISTSNGSLEGLDNQEGGVCCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

Qy          191 GAAHSLEPGKENLPGDPTPSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
                |  :: .|: :| |  :  ::::. .   :   : :::.||:::|  :||::|::  :
Db          194 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIITLVVLLL 253

Qy          251 WRRRRAKPSESRHPGPGSSFGRGGSLGLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                 |||: :||: :      |  |   :       : :||    | ||::||       ::|||
Db          254 KYRRHRHKHSPQHTTTLSLSTLATPKRGGNN-----TADSVFCPH 306

Qy          311 YEKVSGDYGHPVVIVQDGPPQSPNIYYKV 340
                ||||||||||||::|:: |||||.|||||
Db          307 YEKVSGDYGHPVIVQEMPPQSPANIYYKV 336
```

```
RESULT 15
ADYS1238
ID   ADYS1238 standard; protein; 336 AA.
XX
AC   ADYS1238;
XX
DT   19-MAY-2005  (first entry)
XX
DE   Mouse ephrin-B2 SEQ ID NO:7.
XX
KW   ephrin; hematopoiesis; hyperproliferation; cytostatic; antianemic;
KW   antiinflammatory; antipsoriatic; gastrointestinal-gen.; dermatological;
KW   coagulant; immunostimulant; cerebroprotective; vasotropic; antiulcer.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 2..3
FT                   /note= "Optionally deleted"
XX
PN   US2005049194-A1.
XX
PD   03-MAR-2005.
XX
PF   31-OCT-2003;  2003US-00698907.
XX
PR   09-NOV-2001;  2001US-0345206P.
PR   02-JUL-2002;  2002US-0393272P.
PR   08-NOV-2002;  2002US-00291290.
PR   03-APR-2003;  2003US-0460488P.
XX
DR   WPI; 2005-193317/20.
XX
PA   (FRIS/) FRISEN J;
PA   (HOLM/) HOLMBERG J.
XX
PI   Frisen J, Holmberg J;
XX
PT   Use of ephrin and its molecules for alleviating a symptom or a disorder
PT   with reduced levels of hematopoiesis, increased levels of cellular
PT   proliferation in an intestinal tract, or abnormal level of cellular
PT   proliferation in a tissue.
XX
PS   Disclosure; SEQ ID NO 7; 68pp; English.
XX
CC   The invention relates to a novel use of ephrin, ephrin inhibitors, and
CC   ephrin receptors for alleviating a symptom or a disorder having reduced
CC   levels of hematopoiesis, having increased levels of cellular
CC   proliferation in an intestinal tract, or having an abnormal level of
CC   cellular proliferation in a tissue. A composition of the invention has
CC   cytostatic, antianemic, antiinflammatory, antipsoriatic, gastrointestinal
CC   -gen., dermatological, coagulant, immunostimulant, cerebroprotective,
CC   vasotropic, and antiulcer activity. The present sequence represents
CC   murine ephrin-B2.
XX
SQ   Sequence 336 AA;

Query Match             34.5%;  Score 637.5;  DB 9;  Length 336;
Best Local Similarity   42.1%;  Pred. No. 1.8e-43;
Matches  139;  Conservative  49;  Mismatches  129;  Indels  13;  Gaps  5;

Qy           14 GALLLLGVLLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGHSS 73
                |::|   |||||||: ||:||: .||||||:||:|| :::||||||:||||::||:
Db           17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKIV 73

Qy           74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
                |: |||:|   ||| ||||||||||||| |||||||||  ::||:|||:||||||
Db           74 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133

Qy          134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPER-DR 190
                |||| :|::|: |||:: :|||| : |  :|::.|||        .::    ::|: :
Db          134 DYYIISTSNGSLEGLDNQEGGVCCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

Qy          191 GAAHSLEPGKENLPGDPTPSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
                |  :: .|: :| |  :  ::::. .   :   : :::.||:::|  :||::|::  :
Db          194 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIITLVVLLL 253

Qy          251 WRRRRAKPSESRHPGPGSSFGRGGSLGLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
                 |||: :||: :      |  |   :       : :||    | ||::||       ::|||
Db          254 KYRRHRHKHSPQHTTTLSLSTLATPKRGGNN-----TADSVFCPH 306

Qy          311 YEKVSGDYGHPVVIVQDGPPQSPNIYYKV 340
                ||||||||||||::|:: |||||.|||||
Db          307 YEKVSGDYGHPVIVQEMPPQSPANIYYKV 336
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Search completed: December 21, 2005, 14:30:19

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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 14:22:09 ; Search time 20.956 Seconds
(without alignments)
1561.068 Million cell updates/sec

Title: US-10-021-121-4
Perfect score: 1850
Sequence: 1 MGPPHSGPGGVRVGALLILG..........PVYIVQDGPPQSPNIYYKV 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	637.5	34.5	336	2	I49766	hepatoma transmemb
2	632	34.2	346	2	S46693	elk ligand - human
3	629.5	34.0	333	2	I84743	hepatoma transmemb
4	613.5	33.2	345	2	I48780	Stral/Eplg2 protei
5	608.5	32.9	345	2	I58406	LERK-2 - rat
6	214.5	11.6	237	2	T19914	hypothetical prote
7	179	9.7	238	2	I38849	LERK-3 - human
8	176	9.5	209	2	A54984	ELF-1 protein prec
9	175.5	9.5	213	2	JE0322	ephrin-A2 - human
10	170.5	9.2	228	2	A57084	repulsive axon gui
11	169.5	9.2	201	2	I38850	LERK-4 - human
12	167.5	9.1	228	2	I58170	LERK-7 precursor -
13	166	9.0	205	2	A36377	B61 protein precur
14	159	8.6	680	2	S31216	collagen alpha 1(X
15	154.5	8.4	1049	1	CGB07S	collagen alpha 1(I
16	153.5	8.3	1670	1	CGHU3B	collagen alpha 3(I
17	151.5	8.2	301	2	B31219	collagen 2 - Caeno
18	149	8.1	325	2	T32248	hypothetical prote
19	149	8.1	569	2	S42886	collagen - silkwor
20	148.5	8.0	316	2	T20497	hypothetical prote
21	148	8.0	921	2	S42617	collagen alpha 1(I
22	146.5	7.9	1315	2	A56101	collagen alpha 1(X
23	146.5	7.9	1492	2	A40333	collagen alpha 1'(
24	146.5	7.9	1774	2	S20819	collagen alpha 1(X
25	146	7.9	675	2	S20815	collagen alpha 3(I
26	145.5	7.9	305	2	T20906	hypothetical prote
27	145	7.8	674	2	S13301	collagen alpha 1(X
28	145	7.8	931	2	S13580	collagen alpha 1(I
29	144.5	7.8	438	2	S53787	collagen alpha cha
30	144	7.8	1027	2	S28774	collagen alpha cha
31	143	7.7	1747	2	A54121	collagen alpha-4 c
32	142.5	7.7	743	1	S23779	collagen alpha 1(V
33	142.5	7.7	1496	2	CGHU2V	collagen alpha 1(V
34	142	7.7	744	2	S15435	collagen alpha 1(V
35	142	7.7	1029	1	S21369	collagen alpha 2(V
36	142	7.7	1763	1	S16366	collagen alpha 1(I
37	141.5	7.6	1466	1	CGHU7L	collagen alpha 1(I
38	141	7.6	319	2	T32250	hypothetical prote
39	141	7.6	744	1	A34246	collagen alpha 1(V
40	141	7.6	744	1	S23298	collagen alpha 1(V
41	140.5	7.6	305	2	T30165	hypothetical prote
42	140	7.6	304	2	T22482	hypothetical prote
43	140	7.6	680	1	CGHU1D	collagen alpha 1(x
44	139.5	7.5	210	2	B44984	collagen - nematod
45	139	7.5	940	2	JE0291	FB19 protein - hum

ALIGNMENTS

RESULT 1
I49766
hepatoma transmembrane kinase ligand - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49766
R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews,
Proc. Natl. Acad. Sci. U.S.A. 92; 1866-1870, 1995
A;Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine kin
A;Reference number: I49766; MUID:95199254; PMID:7534404
A;Accession: I49766
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-336 <RES>
A;Cross-references: UNIPROT:P52800; UNIPARC:UPI00000020B55; GB:L38847; NID:g769677; PIDN:I
C;Genetics:
A;Gene: HTK

Query Match 34.5%; Best Local Similarity 42.1%; Score 637.5; DB 2; Length 336;
Matches 139; Conservative 49; Mismatches 129; Indels 13; Gaps 5; Pred. No. 1.3e-37;

Qy 14 GALLILGVLGIVSGLSLEPYYWNSANKRFQAEGGYVLLYPQIGDRLDLLCPRARPCGPHSS 73
      |:|| | || |||| :||||| |||||||||||||:||
Db 17 GLIMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLIYPQIGDKLDIICPKV---DSKTV 73

Qy 74 PNYEFYKLYLLVGGAQCRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
      |:| | | :||. | || ||| ||||||||||||:||
Db 74 GQYEYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133

Qy 134 DYYIIATSDGTREGLESLQGGVCLTRGMKYLLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
      ||||||||||:|||||| |||:|:| |||||| .   :
Db 134 DYYIISTSNGSLEGLDNQBGGVCQTRAMKILMKVSGDASSAGSARNHGPTRRPELEAGTN 193

Qy 191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGNAGGLALLLLGVAGAGGAMC 250
      : . | : |: | :
Db 194 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL 253

Qy 251 WRRRAKPSESRHPGPGSFGRGGSLGLGGCGGGMGPREAEPCELGIALRGGGAADPPFCPH 310
Db 254 KYRRHRKHSPQHTTTLSLSTLATPKRGGNN---NGSEPSDVIIPLR---TADSVFCPH 306

Qy 311 YEKVSGDYGHPVYIVQDGPPQSPNIYYKV 340
      ||||||:||| || |||||||||||||
Db 307 YEKVSGDYGHPVYIVQEMPPQSPANIYYKV 336

RESULT 2
S46693
elk ligand - human
C;Species: Homo sapiens (man)
C;Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C;Accession: S46993
R;Beckmann, M.P.; Cerretti, D.P.; Baum, P.; vanden Bos, T.; James, L.; Farrah, T.; Kozlo
EMBO J. 13, 3757-3762, 1994
A;Title: Molecular characterization of a family of ligands for eph-related tyrosine kina
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: I84743
R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews
Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995
A;Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine kin
A;Reference number: I49766; MUID:95199254; PMID:7534404
A;Accession: I84743
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-333 <RES>
A;Cross-references: UNIPROT:P52799; UNIPARC:UPI0000129C9B; GB:L38734; NID:g769675; PIDN:
C;Genetics:
A;Cross-references: GDB:EPLG5; LERK5
A;Gene: GDB:438338; OMIM:600527
A;Map position: 13q33-13q33

Query Match   34.0%; Score 629.5; DB 2; Length 333;
Best Local Similarity   40.9%; Pred. No. 4.5e-37;
Matches 135; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

Qy   14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGHSS 73
          ||| :|| :||| ::|: | |||:||||:||:|:|:|||||||||||||||| :|||
Db   14 GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLIVLYPQIGDKLDIICPKV---DSKTV 70

Qy   74 PNYEFYKLYLVGGAQGRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
          ||:|||||||||||||| ||||||||||||||||||||||:||||||||||||| :||
Db   71 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 130

RESULT 3

I84743
hepatoma transmembrane kinase ligand – human
C;Species: Homo sapiens (man)
A;Accession: I84743
A;Status: preliminary

Query Match   34.2%; Score 632; DB 2; Length 346;
Best Local Similarity   39.5%; Pred. No. 3.2e-37;
Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

Qy   8 PGGVRVGALLLLGVLGLVSGL------------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
         || :|| ||||||||||||||
Db   4 PGQRWLGKWLVAMVWVWALCRLIATPLAKNLEPVSWSSLNPKFLSGKGLIVIYPKIQFS 63

Qy   62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
         ||| |:| :|||||||:|||||||||||||||||||||||||||||||||||||
Db   64 CPRAEAGRP-------YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy   122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLITRGMKVLLRVGQSPRGGAVPRKPV 181
         |||||||||||||||||||||||||||||||||||:||||||:|||:||::|||||||||
Db   119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy   182 SEMPERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
         :| | ||: |:| ||: |||||||||:||| ||| |||:||||||||| | :|
Db   179 SRPSKEADNTVKWATQAPGSRGSLGDSDGKHETVNQEEKSGP------- 231

Qy   237 ------LLILGVAGAGGA--------------MCWRRRAKPSESRHPGPGSFGRGGSLGL 277
               |:|:|| |||| |:|||||||||||||:|||:|||||| |||
Db   179 SRPSKEADNTVKWATQAPGSRGSLGDSDGKHETVNQEEKSGP------- GASGGSSGDPD 231

Qy   278 ---GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
         ||||||||||:|||||||||||:|:|:||:
Db   283 STLASPKGGSGTAGTEPSDIIIPLR----TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339

Qy   334 PNIYYKV 340
         ||||||
Db   340 ANIYYKV 346

RESULT 4

I48780
Stal/Eplg2 protein – mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
A;Accession: I48780; A55507; A55062; S52670
R;Fletcher, F.A.; Renshaw, B.; Hollingsworth, T.; Baum, P.; Lyman, S.D.; Jenkins, N.A.; C
Genomics 24, 127-132, 1994
A;Title: Genomic organization and chromosomal localization of mouse Eplg2, a gene encodi
A;Reference number: A55507; MUID:95203867; PMID:7896266
A;Accession: A55507
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-345 <FLE>
A;Cross-references: UNIPARC:UPI00000018AC; GB:U07598

R;Shao, H.; Lou, L.; Pandey, A.; Pasquale, E.B.; Dixit, V.M.
J. Biol. Chem. 269, 26606-26609, 1994
A;Title: cDNA cloning and characterization of a ligand for the Cek5 receptor protein-tyr
A;Reference number: A55062
A;Accession: A55062
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-89, T', 91-345 <SHA>
A;Cross-references: UNIPARC:UPI00001GCADF; GB:U12983; NID:9575928; PIDN:AAA53231.1; PID:
A;Accession: A55507
C;Genetics:
A;Gene: EPLG2

Query Match   33.2%; Score 613.5; DB 2; Length 345;
Best Local Similarity   38.2%; Pred. No. 6.3e-36;
Matches 138; Conservative 51; Mismatches 107; Indels 65; Gaps 10;

Qy   15 ALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGHS 72
          ||||||:||||||| |||||||||||||||||||||||||||||||||||||||| :|
Db   15 AMVVLTLCRLIATPLAKNLEPVSWSSLNPKFLSGKGLIVIYPKIQFS 72

Qy   73 SPNYEFYKLYLVGGAQGRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSH 132
          |:|||||||||:||||||||||||||||||||||||||||||:|||||||||||:|:||
Db   73 ---YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPHQEIRFTIKFQEFSPNYMGLEFKKY 129

Qy   133 HDYYIIATSDGTREGLESLQGGVCLITRGMKVLLRVGQD------LPPPSMPAVAGAAGGP------LA 193
          ||||| ||:|||:|||:||:|||| :|||||:|::||||| || ||:||||||||
Db   130 HDYITSTSNGSLEGLENREGGVCRTRTMKIVMKVGQD-NAVTPEQLTTSRPSKESDNT 188

Qy   193 AHSLEPGKENLPGDPTSNATSRGAEGP------LPPPSMPAVAGAAGG------LA 236
Db   193 LA 236

Qy   311 YEKVSGDYGHPVYIVQDGPPPSPPNIYYKV 340
         |||||||||||||||||| || |||||||||
Db   304 YEKVSGDYGHPVYIVQEMPPQSPANIYYKV 333

Db   71 GQYEYYKVRVMVDKDQADRCTIKKENTPLLNCAKPDQDIRFTIKFQEOFSPNLWGLLEFQKNK 130
            :||:|:|:| |:| || |||:||: ||||: :
Db   131 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Db   191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
Db   191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSSEVALFAGIASGCCIIFIVIILLVLLL 250

Db   251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFPCH 310
Db   251 KYRRHRHKRHSPQHTTTLSLSTLATPKRSGNN----NGSEFSDIIIPLR---TADSVFCPH 303

RESULT 5

I58406
LERK-2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I58406
R;Fletcher, F.A.; Carpenter, M.; Shilling, H.; Baum, P.; Ziegler, S.; Gimpel, S.; Hollin...
Oncogene 9, 3241-3248, 1994
A;Title: LERK-2, a ligand for the receptor tyrosine kinase ELK, is evolutionarily conser...
A;Reference number: I58406; MUID:95022634; PMID:7936648
A;Accession: I58406
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-345 <RES>
A;Cross-references: UNIPROT:P52796; UNIPARC:UPI0000129C98; EMBL:U07560; NID:g563118; PID...
C;Genetics:
A;Gene: Eplg2

Query Match   32.9%; Score 608.5; DB 2; Length 345;
Best Local Similarity   38.0%; Pred. No. 1.4e-35;
Matches 137; Conservative 52; Mismatches 107; Indels 65; Gaps 10;

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Qy  15 ALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHS 72
Db  15 AMVVLTLCRLATPLAKNLEPVSWSSLNPKFLSGKGLVTYPKIGDKLDIICPRAEAGR--  72

Qy  73 SPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSH 132
Db  73 ---YEYYKLYLVRPEQAAACSTVLDPNVLVTCNKPQQEIRFTIKFQEFSPNYMGLEFKKY 129

Qy 133 HDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGA 192
Db 130 HDYYITSTSNGSLEGLENREGGVCRTRTMKIVMKVGQDP-NAVTPEQLTTSRPSKESDNT 188

Qy 193 AHSLEPGKENLPGDPTSNATSRGAEGP------LPPPSMPAVAGAAGG------LA 236
Db 189 VKT--------ATQAPGRGSQGDSDGKHETVNQEEKSGPGAGGGGSGSGGDSDSFPNSK 236

Qy 237 LILLLGVLGVAGGA-------MCWRRRRAKPSESRHPGPSFSGRGGSLGL----GG 279
Db 237 VALFAAVGAGCVIFLLIIIFLTVLLLKURKRHRKHTQQ------RAAALSLSTLASP 287

Qy 280 GGGMGPREAEPGELGIALRGGGAADPPPCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYK 339
Db 288 KGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVVIVQEMPPQSPANIYYK 344

Qy 340                                                            V 340
Db 345                                                            V 345
```

RESULT 6

T19914
hypothetical protein C43F9.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19914
R;Mortimore, B.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19195
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: T19914
A;Molecule type: DNA
A;Residues: 1-237 <WIL>
A;Cross-references: UNIPROT:Q9U3M2; UNIPARC:UPI000000078016; EMBL:Z82262; PIDN:CAB54195.1;
A;Experimental source: clone C43F9
C;Genetics:
A;Gene: CESP:C43F9.8
A;Map position: 4
A;Introns: 32/2; 96/3; 214/1

Query Match   11.6%; Score 214.5; DB 2; Length 237;
Best Local Similarity   25.7%; Pred. No. 4.1e-08;
Matches 53; Conservative 41; Mismatches 83; Indels 29; Gaps   6;

```
Qy  11 VRVGALLLLGVLGLVS-GLSLEPVYWNSANKRFQAEG-GVVLYPQIGDRLDLLCPRARPP 68
Db   1 MQIATFILLSLFPFIGWARKIPDINWISSNPIFDVSNTDHVISVHIGDRVSIRCPKSDET 60

Qy  69 GPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHE 128
Db  61 G-----KYEYSYIYMVSDEEYDHCFL-SKPRLVGACDNQTINASINIVFRSFTPTPGGFE 114

Qy 129 FRSHHDYYIIA-------------TSDGTREGLESLQGGVCLTRGMKVLLRVGQ 169
Db 115 FQPGKNYFLISKSEVDALIIYETANQIFPGCTSDGTLEGIDRKKDGLCTAPKQMKIKFEVGQ 174

Qy 170 SPRGGAVPRKPVSEMPMERDRGAAHS 195
Db 175 DRRGIENPK--FAARTLKXDRDAEHS 198
```

RESULT 7

I38849
LERK-3 - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.; Lyman, S.D.; ...
Oncogene 10, 299-306, 1995
A;Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs encodi...
A;Reference number: I38849; MUID:95140419; PMID:7838529
A;Accession: I38849
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-238 <RES>
A;Cross-references: UNIPROT:P52797; UNIPARC:UPI000129C8F; EMBL:U14187; NID:g642832; PIDN...
C;Genetics:
A;Gene: GDB:438336; OMIM:601381
A;Gene: GDB:EPLG3
A;Cross-references: UNIPROT:P52797; UNIPARC:UPI000129C8F; EMBL:U14187; NID:g642832; PIDN
A;Map position: 1q21-1q22
A;Superfamily: axon guidance signal protein

Query Match   9.7%; Score 179; DB 2; Length 238;
Best Local Similarity   28.4%; Pred. No. 1.3e-05;
Matches 65; Conservative 24; Mismatches 80; Indels 60; Gaps 12;

```
Qy   7 GPGGVRGALILLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCP--R 64
Db  24 GPG------------GALG------NRHAVVWNSSNQHRRE-GYTVQVNNANDYLDIYCPHYN 67

Qy  65 ARPPGPHSSP---NYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKF 117
Db  68 SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFK-RWECNRPHAPHSPIKFSEKF 126

Qy 118 QEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVP 177
Db 127 QRYSAFSLGYEFHAGHEYYYISTPTHNLH------WKCLR--MKVFVCCASTSHSG--- 174

Qy 178 RKPVSEMP-------------MERDRGAAHSLE------PGKENLP 204
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RESULT 8
A54984

Db   175 EKPVPTLPQFTMGPNVKINVLEDPEGENPQVPKLEKS1SGTSPKREHLP 223
              |:| :|:|:|

C;Accession: A54984; A55873
R;Cheng, H.J.; Flanagan, J.G.
A54984
N;Alternate names: Cek7 ligand
C;Species: Mus musculus (house mouse)
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 09-Jul-2004
A;Reference number: A54984; MUID:95007776; PMID:7522971
A;Cross-references: UNIPROT:P52801; UNIPARC:UPI0000020CE3; GB:U14941; NID:g558836; PIDN:
A;Molecule type: mRNA
A;Residues: 1-209 <CHE>
A;Status: preliminary
C;Accession: A54984
A;Title: ELF-1 protein precursor - mouse
R;Cell 79, 157-168, 1994
C;Reference number: A54984; MUID:95007776; PMID:7522971
A;Title: Identification and cloning of ELF-1, a developmentally expressed ligand for the

RESULT 9
JE0322
ephrin-A2 - human

Db   175 EAPEPIFTSNSSCSGLGG 192
              |||:|:||
Qy   205 GDP----TSNATSRGAEG 218
              :|||||
Qy   152 ----PNLVDRPCLR--LKYYVR--------------PTNEFLY 174
              |||:|| :|| :::|: ::|:
Qy   145 REGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLP 204
              ||:|:||||||||||||||||||| :|:| ||:||:||:||:::|||:||:||
Db   94 GHASCDHRQRGFKRWECNRPAAPGGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATP-- 151
              :: ||||||||||||||||||||||||||||||||||||:||:||:|:|||
Qy   88 QGRRCEAPPAPNLLLTCDRPDL----DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGT 144
              ||||:||||||||||||||||| |||::|||::::|:|:|:|||:||:::|
Db   35 VYWNRSNPRFQVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE 93
              ||| ||| :|| ||::::||||||::|||::|| ::|| :::||:|:|:|:||:||
Qy   33 VYWNSANKRFQAE------GGYVLYPQIGDRLDLLCPRARPPGPHSSSPNYEFYKLYLVGGA 87

Query Match   29.3%; Score 176.5; DB 2; Length 209;
Best Local Similarity   19; Pred. No. 1.8e-05;
Matches   58; Conservative   19; Mismatches   69; Indels   52; Gaps   7;

C;Keywords: lipoprotein; membrane protein
C;Superfamily: axon guidance signal protein
A;Cross-references: UNIPARC:UPI000000020CE3; GB:U14752; NID:g681886; PIDN:AAA68520.1; PID:
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-209 <SHA>
A;Accession: A55873
A;Reference number: A55873; MUID:95181289; PMID:7876076
A;Title: cDNA cloning and characterization of a Cek7 receptor protein-tyrosine kinase li
J. Biol. Chem. 270, 3467-3470, 1995
R;Shao, H.; Lou, L.; Pandey, A.; Verderame, M.F.; Siever, D.A.; Dixit, V.M.

RESULT 10
A57084
repulsive axon guidance signal protein RAGS precursor - chicken

Db   98 GHASCDHRQRGFKRWECNRPAAPGGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISAT 154
              :: ||||||||||||||||||||||||||||||||||||:||:||:|:|||:
Qy   88 QGRRCEAPPAPNLLLTCDRPDL----DLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS 141
              ||||:||||||||||||||||| |||::|||::::|:|:|:|||:||:::|
Db   39 VYWNRSNPRFHAGAGDDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMEHYVLYMVNGE 97
              ||| ||| :| |:::::||||||::|||::|| ::|| :::||:|:|:|:||:||
Qy   33 VYWNSANKRFQA-------EGGYVLYPQIGDRLDLLCPRARPPGPHSSSPNYEFYKLYLVGGA 87

Query Match   9.5%; Score 170.5; DB 2; Length 228;
Best Local Similarity   28.9%; Pred. No. 4.8e-05;
Matches   73; Conservative   30; Mismatches   91; Indels   59; Gaps   13;

F;1-20/Domain: signal sequence #status predicted <SIG>
C;Keywords: glycoprotein; phosphatidylinositol linkage
C;Superfamily: axon guidance signal protein
A;Cross-references: UNIPROT:P52804; UNIPARC:UPI000000129C92; GB:X90377; NID:g1061113; PIDN:
A;Residues: 1-228 <DRE>
A;Molecule type: mRNA
A;Status: preliminary; not compared with conceptual translation
A;Accession: A57084
A;Reference number: A57084; MUID:95360980; PMID:7634326
A;Title: In vitro guidance of retinal ganglion cell axons by RAGS, a 25 kDa tectal prote
Cell 82, 359-370, 1995
R;Drescher, U.; Kremoser, C.; Handweker, C.; Loeschinger, J.; Noda, M.; Bonhoeffer, F.
C;Accession: A57084
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Species: Gallus gallus (chicken)
A57084

RESULT 11
I38850
LERK-4 - human

Db   215 LATLLFLLAMLLI 227
              |:|| :| ::|:
Qy   228 VAGRAGGLALLLL 240
              |:|| ::|:|:|
Db   160 -PANSCMKTIGVHDRVFDVDNDKVENSLEPADDTV---RESAEPSRG-ENAAQTPRIPIRL 214
              ||::: |:|: | :|| ::||:|:::|:|:| : |:| |:|| :|::|:|
Qy   170 SPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMP--A 227
              :|:|||||||||||||||||||||||||||||:|:|:| :|||||||::|| :|| :
Db   114 FSEKFQLFTPFSLGFEFRPGREYFYISSAIPDNGRRS---------CLK--LKVFVR--- 159
              ||::||:||:|||:|:|| :|::|::: ::|:||:: ||: ||:|:|
Qy   114 FTIKFQEYSPNLWGHEFRSHHDYYIIATS---DGTREGLESLQGGVCLTRGMKVLLRVGQ 169
              || :||:|: ||:|:|:: |::||: :|||: ::|:||:||||:||||:||:||:||:
Db   65 YEDSVPEDKT--ERYVLIMVNFDGYSSCDHISKGFKRWECNRPHSPN----------GPLK 113
              |:||:| :: ||::|:|:|: ||::|:| ||||||||||:|| ||||
Qy   65 ARPGPHSSPNYEFYKLYLVG----------GAQGRRCEAPPAPNLLLTCDRPDLDLR 112
              :||| ||:::|:|:|:|:| ||:|||||||||||||||||||||||||
Db   6 MLLLAVAALWVCVRGQEPGRKAVADRYAYVYWNSTNPRFQ-QGDVHIDVCINDVLDVFCPH 64
              |:| ::|:|||:::|:|:|: |:::||| ||||:|||:|| |:| :|: :|::|:|| |
Qy   16 LILILGVLGL-VSGLSLEP------------VYWNSANKRFQAEGGYVLYPQIGDRLDLLLCPR 64

Query Match   9.2%; Score 170.5; DB 2; Length 228;
Best Local Similarity   28.9%; Pred. No. 4.8e-05;
Matches   73; Conservative   30; Mismatches   91; Indels   59; Gaps   13;

A;Map position: 1q21-1q22
A;Genetics:
A;Cross-references: GDB:438337; OMIM:601380
A;Gene: GDB:EPLG4
C;Genetics:
A;Cross-references: UNIPROT:P52798; UNIPARC:UPI000000129C90; EMBL:U14188; NID:g642834; PIDN
A;Residues: 1-201 <RES>
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: I38850
A;Reference number: I38849; MUID:95140419; PMID:7838529
A;Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs encodi
Oncogene 10, 299-306, 1995
R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.; Lyman, S.D.; S
C;Accession: I38850
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Species: Homo sapiens (man)
I38850

A;Superfamily: axon guidance signal protein
A;Cross-references: UNIPROT:O43921; UNIPARC:UPI000016A442; GB:AJ007292; NID:g3689367; PID
A;Residues: 1-213 <AAS>
A;Molecule type: mRNA
A;Status: preliminary
A;Accession: JE0322
A;Reference number: JE0322; MUID:99045414; PMID:9826538
A;Title: Cloning, chromosomal mapping, and tissue expression of the gene encoding the huma
Biochem. Biophys. Res. Commun. 252, 378-382, 1998
R;Aasheim, H.; Pedeutour, F.; Grosgeorge, J.; Logtenberg, T.
C;Accession: JE0322
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
C;Species: Homo sapiens (man)

Query Match   9.5%; Score 175.5; DB 2; Length 213;
Best Local Similarity   36.8%; Pred. No. 2e-05;
Matches   43; Conservative   14; Mismatches   51; Indels   9; Gaps   3;

C;Superfamily: axon guidance signal protein

Query Match   9.2%; Score 169.5; DB 2; Length 201;
Best Local Similarity   29.9%; Pred. No. 5e-05;
Matches 66; Conservative 18; Mismatches 82; Indels 55; Gaps 10;

```
Qy   24  LVSGLSL--EPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSSPNYEFYKLY   82
             ||||||  :|||||||||||||||||||||||||||||:||:||:||
Db   20  LRGGSSLRHVVYWNSSNPRL-LRGDAVVELGLNDYLDIVCPHYEGPGPPEGP--ETFALY   76

Qy   83  LVGGAQGRRCEAP-PAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS  141
Db   77  MVDWPGYESCQAEGPRAYXRWVCSLPGHVQFSEKIQRFTPFSLGFEFLPGETYYISVP  136

Qy  142  DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPEMRDRGAAHSLEPGKE  201
Db  137  --TPE-----SSGQCL     RLQVSVCCKERKSESAHPV-----  164

Qy  202  NLPGDPTSNATS--RGAEGPLPPPSMPAVAGAGAGGLALLLLL  240
Db  165  ---GSPGESGGTSGWRGGGDTPSP----LCLLLL  189
```

RESULT 12
I58170
LERK-7 precursor - human
N;Alternate names: AL-1
C;Species: Homo sapiens (man)
R;Kozlosky, C.J.; VandenBos, T.; Park, L.S.; Cerretti, D.P.; Carpenter, M.K.
R;submitted to the EMBL Data Library, May 1995
C;Accession: I58170; G01812
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
R;Reference number: G08477
R;Winslow, J.W.; Moran, P.; Valverde, J.; Shih, A.; Yuan, J.Q.; Wong, S.C.; Tsai, S.P.;
Neuron 14, 973-981, 1995
A;Title: Cloning of AL-1, a ligand for an Eph-related tyrosine kinase receptor involved
A;Accession: I58170
A;Molecule type: mRNA
A;Reference number: I58170; MUID:95267434; PMID:7748564
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: I58170
A;Molecule type: mRNA
A;Residues: 1-228 <KO2>
A;Cross-references: UNIPROT:P52803; UNIPARC:UPI0000129C93; GB:S77167; NID:g914184; PID:g
A;Cross-references: UNIPARC:UPI0000129C93; EMBL:U26403; NID:g1019430; PIDN:AAB60377.1; P

Query Match   9.0%; Score 166; DB 2; Length 205;
Best Local Similarity   27.5%; Pred. No. 8.9e-05;
Matches 46; Conservative 31; Mismatches 74; Indels 16; Gaps 5;

C;Superfamily: axon guidance signal protein

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Qy   18  LLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPN--   75
             ||||:||:||:||||||||:|:||||||||||||||||||:|||:||||:
Db    8  LLGLCCSLAAADRHTVFWNSSNPKFRNE-DYTIHVQLNDYVDIICPHYE---DHSVADA   63

Qy   76  YEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL--DLRFTIKFQEYSPNLWGHEFRSH  132
Db   64  MEQVILYLVEHEETYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKRQRFTPTLGKFKEG  123

Qy  133  HDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK  179
Db  124  HSYYISKPIHQHEDR-------CLRLKVTVSGKITHSPQAHVNHQE  163
```

RESULT 13
A36377
B61 protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C;Accession: A36377
R;Holzman, L.B.; Marks, R.M.; Dixit, V.M.
Mol. Cell. Biol. 10, 5830-5838, 1990
A;Title: A novel immediate-early response gene of endothelium is induced by cytokines and
A;Reference number: A36377; MUID:91042512; PMID:2233719
A;Accession: A36377
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-205 <HOL>
A;Cross-references: UNIPROT:P20827; UNIPARC:UPI0000129C89; GB:M57730; NID:g17...

Query Match   9.1%; Score 167.5; DB 2; Length 228;
Best Local Similarity   28.8%; Pred. No. 7.9e-05;
Matches 65; Conservative 29; Mismatches 81; Indels 51; Gaps 11;

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Qy   33  VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSSPNYEFYKLYLYVG------   85
             |||||:|:||  ||||:||||||||:||||||||:||||||||:
Db   34  VYWNSSNPRFQ-RGDYHIDVCINDYLDVPCPHYEDSVPEDKT--ERYVLYMVNFDGYSAC   90

Qy   86  -----GAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIAT  140
Db   91  DHTSKGFKRWECNRPHSEN----GPLKFESEKFQLFTPFSLGFEFRPGREYFYISS  141

Qy  142  AIPDNGRRS---------CLK--LKVFVR----PTNSCMKTIGVHDRVFDVNDKVENSLE  186
Db  141  S---DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPEMRDRGAAHSLE  197

Qy  187  PADDTV--HESAEPSRG-ENAAQTPRIPSRL----LAILLFLLA  223
Db  198  PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAGAGGLALLLLGVA  243
```

RESULT 14
S31216
collagen alpha 1(X) chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S31216; S28807; S22215; S30127; I48299; S26397; S31830
R;Kong, R.Y.C.; Kwan, K.M.; Lau, E.T.; Thomas, J.T.; Boot-Handford, R.P.; Grant, M.E.; Ch
Eur. J. Biochem. 213, 99-111, 1993
A;Title: Intron-exon structure, alternative use of promoter and expression of the mouse c
A;Accession: S28807
A;Molecule type: DNA
A;Residues: 1-680 <KON>
A;Cross-references: UNIPROT:Q05306; UNIPARC:UPI0000026913; EMBL:X67348; NID:g50480; PIDN:CAA47763.1; PIDN
R;Elima, K.; Eerola, I.; Rosati, R.; Metsaeranta, M.; Garofalo, S.; Peraelae, M.; de Cron
Biochem. J. 289, 247-253, 1993
A;Title: The mouse collagen X gene: complete nucleotide sequence, exon structure and exp
A;Reference number: S28807; MUID:93143676; PMID:8424763
A;Accession: S31216
A;Molecule type: DNA
A;Residues: 1-285,'A',287-680 <ELI>
A;Cross-references: UNIPROT:Q05306; UNIPARC:UPI000016CBAA; EMBL:Z21610; NID:g947793; PIDN:CAA47741.1; PID
R;Elima, K.; Eerola, I.; Rosati, R.; Metsaeranta, M.; Garofalo, S.; Peraelae, M.; de Cron
Biochim. Biophys. Acta 1130, 78-80, 1992
A;Title: Specific hybridization probes for mouse alpha-2(IX) and alpha-1(X) collagen mRN
A;Reference number: S22215; MUID:92182017; PMID:1543751
A;Accession: S22215
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 385-450,'K',452-627 <ELA>
A;Cross-references: UNIPROT:UPI000016CBAB; EMBL:X63013; NID:g49795; PIDN:CAA44741.1; PID
R;Apte, S.S.; Olsen, B.R.
Matrix 13, 165-179, 1993
A;Title: Characterization of the mouse type X collagen gene.
A;Reference number: S30127; MUID:93261348; PMID:8492743
A;Accession: S30127
A;Status: preliminary
A;Molecule type: mRNA

A;Residues: 1-12, 'F',14-26,'S',28-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'L'
A;Cross-references: UNIPARC:UPI000017733E5
R;Apte, S.S.; Seldin, M.F.; Hayashi, M.; Olsen, B.R.
Eur. J. Biochem. 206, 217-224, 1992
A;Title: Cloning of the human and mouse type X collagen genes and mapping of the mouse t
Hoppe-Seyler's Z. Physiol. Chem. ; MUID:92267014; PMID:1587271
A;Accession: I48299
A;Molecule type: DNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: protein
A;Residues: 52-247, 'L',249-285, 'A',287-305, 'F',307-416, 'S',418-499, 'L',501-566,'C',568,'
A;Cross-references: UNIPARC:UPI00001CCCAC; EMBL:X65121; NID:g50482; PIDN:CAA46237.1; PID
A;Cross-references: 'SDGYFSQ',24-26,'KQ' <SUM>
A;Accession: S26397
J. Biol. Chem. 263, 581-587, 1988
R;Summers, T.A.; Irwin, M.H.; Mayne, R.; Balian, G.
A;Title: Monoclonal antibodies to type X collagen. Biosynthetic studies using an antibod
A;Reference number: S26397; MUID:88087150; PMID:2826450
A;Gene: Col10a-1
A;Genetics:
A;Map position: 10
A;Introns: 51/3
C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-680/Product: collagen alpha 1(X) chain #status predicted <MAT>
F;553-679/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 8.6%; Score 159; DB 2; Length 680;
Best Local Similarity 25.5%; Pred. No. 0.001;
Matches 97; Conservative 30; Mismatches 108; Indels 146; Gaps 24;

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Qy      1 MGPPHSGPGGV-RVGALLLGVLGLVSGLSLEPVYWNSANKRFQAEGGVVLYPQIGDRLD 59
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Db      1 IGPP--GPSGVGVRRGENGFPGQPGI-----------------------KGDRGFPGEMG 244

Qy    211 LLCPRARPPGPHSSPNYEFYKLYLVGGAGGRRCEAPPAPNLLLTCDRPDLDLRFTIKFCE 119
           ::  :         :                      :        :   ::
Db    245 -----PSGPPGPQGPP------GKQGR--EGIGKPGAIGSPGQPGI------ 277

Qy    120 YSPNLWGHEFRSHHDYYIIATSDGT-----REGLESLQGGVCLTRGMKVLLRVGQSPRGGA 175
           :  :::        ::          :::  : :         :      ::  :
Db    278 --PGEKGHPGSPG-----IAGPGPAPGFGKQGLPGLRG-----QRG------PAG-- 314

Qy    176 VPRKPVSEMPERDRGAAHSLEPGKENLPGDPTPSNATSRGAEGPLPPPSMPAVAGAAGGL 235
            :  :          ::       :       : :          :  :  :: ::
Db    315 LPGAPGA----KGERGPAG---HPGEPGLPGSP---GNMGPQGPKGIPGNHGIPGAKGEI 364

Qy    236 ALLLLGVAGAGGAMCWRRRRAKP------SESRHPG----------PGSFGRGGSLCLGGGGG 282
           ::   :           ::     :::           :::
Db    365 G----LVGPAGPPGA----RGARGPGLDGKIGYPGEPGLNGPKGNPGLPGQKGDPGVGGTPG 419

Qy    283 M----------------GPREAEPGELGIALRGGGAADPFFCPHYEKVSGDYGHPVY 323
                               :::   :
Db    420 LRGPVGPVGAKGVPGHNGEAGPR-GEPGIPGTR----GPTGPGPGVPGFPGSKGDPGNP-- 472

Qy    324 IVDGP---------------PQSPP 334
                                ::::
Db    473 -GAPGPPAGIATKGLNGPTGPP 492
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RESULT 15
CGBO7S
collagen alpha 1(III) chain - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C;Accession: A02862; A38001; A38002; A38003; A38004; A38005; S71946
R;Fietzek, P.P.; Allmann, H.; Rauterberg, J.; Henkel, W.; Wachter, E.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 809-820, 1979
A;Title: The covalent structure of calf skin type III collagen. I. The amino acid sequen
A;Accession: A02862; MUID:80026026; PMID:488906

A;Molecule type: protein
A;Residues: 1-242 <FIS>
A;Cross-references: UNIPROT:P04258; UNIPARC:UPI0000177733E5
R;Dewes, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 821-832, 1979
A;Title: The covalent structure of calf skin type III collagen. II. The amino acid sequer
A;Accession: A38001; MUID:80026027; PMID:488907
A;Molecule type: protein
A;Residues: 243-422 <DEW1>
A;Cross-references: UNIPARC:UPI0000177B8B
R;Dewes, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 833-840, 1979
A;Title: The covalent structure of calf skin type III collagen. III. The amino acid seque
A;Reference number: A38002; MUID:80026028; PMID:488908
A;Molecule type: protein
A;Residues: 423-571 <BEN>
A;Cross-references: UNIPARC:UPI0000177B8C
R;Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 841-850, 1979
A;Title: The covalent structure of calf skin type III collagen. IV. The amino acid seque
A;Reference number: A38003; MUID:80026029; PMID:488909
A;Molecule type: protein
A;Residues: 572-808 <LAN>
A;Cross-references: UNIPARC:UPI0000177B8D
R;Dewes, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 851-860, 1979
A;Title: The covalent structure of calf skin type III collagen. V. The amino acid sequen
A;Accession: A38004; MUID:80026030; PMID:488910
A;Molecule type: protein
A;Residues: 809-947 <DEW2>
A;Cross-references: UNIPARC:UPI0000177B8E
R;Allmann, H.; Fietzek, P.P.; Glanville, R.W.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 861-868, 1979
A;Title: The covalent structure of calf skin type III collagen. VI. The amino acid
A;Accession: A38005; MUID:80026031; PMID:488911
A;Molecule type: protein
A;Residues: 948-1049 <ALL>
A;Cross-references: UNIPARC:UPI0000177B8F
A;Experimental source: skin
R;Henkel, W.
Biochem. J. 318, 497-503, 1996
A;Title: Cross-link analysis of the C-telopeptide domain from type III collagen.
A;Reference number: S71946; MUID:96404897; PMID:8809038
A;Accession: S71946
A;Molecule type: protein
A;Residues: 87-106;1017-1029;1037-1049 <HEN>
A;Cross-references: UNIPARC:UPI0000173B90; UNIPARC:UPI0000173B91; UNIPARC:UPI0000173B92
C;Comment: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hy
C;Comment: The type III collagen molecule is a trimer of identical chains, linked to eac
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology
C;Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyprolin
F;1-1049/Product: collagen alpha 1(III) chain #status experimental <CAB>
F;1-14/Region: amino-terminal nonhelical telopeptide
F;15-1040/Region: helical
F;587-589/Region: cell attachment (R-G-D) motif
F;752-754/Region: cell attachment (R-G-D) motif
F;875-877/Region: cell attachment (R-G-D) motif
F;878-880/Region: cell attachment (R-G-D) motif
F;935-937/Region: cell attachment (R-G-D) motif
F;1041-1049/Region: carboxyl-terminal nonhelical telopeptide
F;95,107,119,938,950/Modified site: allysine (Lys) #status predicted
F;107,950/Modified site: 5-hydroxylysine (Lys) #status experimental
F;107/Binding site: carbohydrate (Lys) (covalent) #status predicted
F;1040,1041/Disulfide bonds: interchain #status predicted

Query Match 8.4%; Score 154.5; DB 1; Length 1049;
Best Local Similarity 26.5%; Pred. No. 0.0034;
Matches 60; Conservative 9; Mismatches 74; Indels 83; Gaps 8;

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Qy   171  PRGGAVPRKPVSEMPMERDRGA-----------------------AHSLEPGKEN  202
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Db   688  PAGGSGPAGPPGQGVKGERGSPGGPGAAGFPGGRGPPPGSNGNPGPPGSSGAPGKDG  747

Qy   203  LPGDPTSNAT-----------------SRGAEGPLPPPSMPAVAGAAGGLALLLGVAGA  245
          |||  |||                    |||
Db   748  PPGPPGSNGAPGSPGISGPKGDSGPPGERGAPGGPQGPPGAPGPLGIAG-----LTGARGL  802

Qy   246  GGAMCWRRRRAKP------SESRHPGP-------GSFGRGGSLGLGGGGGMGPREAEPGE  292
             |   |:          ||||                  :|                  ||
Db   803  AGPPGMPGGARGSPGPQGIKGENGKPGPSGQNGERGPPGPQGLPGLAGTRAGEPGRDGNPGS  862

Qy   293  LGIALRGG-------GAADPPPCPHYEKVSGDYGHPVYIVQDGPP  330
             |:              |||                        |||
Db   863  DGLPGRDGAPGAKGDRGENGSPGAP-------GAPGHP------GPP  896
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Search completed: December 21, 2005, 14:36:32
Job time : 21.956 secs

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OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: December 21, 2005, 14:21:53 ; Search time 131.723 Seconds
(without alignments)
1821.088 Million cell updates/sec

Title: US-10-021-121-4
Perfect score: 1850
Sequence: 1 MGPPHSGPGGVRVGALILLG.........PVYIVQDGPPQSPPNIYKV 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 70528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1850	100.0	340	1	Q15768	EFNB3_HUMAN homo sapien
2	1780	96.2	340	1	Q35393	EFNB3_MOUSE mus musculu
3	1780	96.2	340	1	Q5F221	EFNB3_MOUSE mus musculu
4	923	49.9	331	2	Q90231	Q90231_BRARE brachydanio
5	923	49.9	342	2	Q50203	Q50203_BRARE brachydanio
6	919	49.7	327	2	Q9PT69	Q9PT69_XENLA xenopus lae
7	637.5	34.5	336	1	P52800	EFNB2_MOUSE mus musculu
8	637.5	34.5	336	1	Q4FJM3	Q4FJM3_MOUSE mus musculu
9	632	34.2	346	1	P98172	EFNB1_HUMAN homo sapien
10	629.5	34.0	333	1	P52799	EFNB2_HUMAN homo sapien
11	629.5	34.0	333	2	Q5JV56	Q5JV56_HUMAN homo sapien
12	629.5	34.0	333	2	Q9PU04	Q9PU04_CHICK gallus gall
13	628	33.9	334	1	O73612	O73612_CHICK gallus gall
14	626.5	33.9	332	2	O73874	O73874_BRARE brachydanio
15	616	33.3	341	2	Q90233	Q90233_BRARE brachydanio
16	615.5	33.3	345	2	Q6P7B6	Q6P7B6_RAT rattus norv
17	613.5	33.2	345	1	P52795	EFNB1_RAT rattus norv
18	613.5	33.2	345	1	P52796	EFNB1_MOUSE mus musculu
19	608.5	32.9	329	2	Q5419	Q5419_MOUSE mus musculu
20	605.5	32.7	334	2	Q6PF53	Q6PF53_XENLA xenopus lae
21	605.5	32.7	327	2	Q90232	Q90232_BRARE brachydanio
22	600	32.4	324	1	O13097	EFNB1_XENLA xenopus lae
23	568.5	30.7	204	2	Q4SHZ6	Q4SHZ6_TETNG tetraodon n
24	452	24.4	386	2	Q47D5	Q47D5_TETNG tetraodon n
25	401	21.7	204	2	Q4RK83	Q4RK83_TETNG tetraodon n
26	349.5	18.9	359	2	Q4H318	Q4H318_CIOIN ciona intes
27	341.5	18.5	217	2	Q5JV57	Q5JV57_HUMAN homo sapien
28	340	18.4	205	2	Q9W6H9	Q9W6H9_XENLA xenopus lae
29	251.5	13.6	97	2	Q4RDZ1	Q4RDZ1_TETNG tetraodon n
30	239.5	12.9	212	2	Q61WH3	Q61WH3_CAEBR caenorhabdi
31	234	12.6	218	2	Q9U3M2	Q9U3M2_CAEEL caenorhabdi
32	214	11.6	182	2	Q4RT95	EFNA5_TETNG tetraodon n
33	198.5	10.7	279	2	Q9U474	Q9U474_CAEEL caenorhabdi
34	198	10.7	278	2	Q61HF9	Q61HF9_CAEBR caenorhabdi
35	195	10.5	195	1	P79727	EFNA2_BRARE brachydanio
36	184.5	10.0	428	2	Q5TXC6	Q5TXC6_ANOGA anopheles g
37	182	9.8	260	2	Q6VU49	Q6VU49_MANSE manduca sex
38	182	9.8	652	2	Q9V4E1	Q9V4E1_DROME drosophila
39	179	9.7	238	1	P52797	EFNA3_HUMAN homo sapien
40	178.5	9.6	202	2	Q98TZI	Q98TZI_CHICK gallus gall
41	176	9.5	209	1	P52801	EFNA2_MOUSE mus musculu
42	175.5	9.5	202	1	P52800	EFNA2_HUMAN homo sapien
43	172.5	9.3	217	2	Q5M7P3	Q5M7P3_XENTR xenopus tro
44	172	9.3	200	1	O43921	EFNA2_CHICK homo sapien
45	170.5	9.2	228	1	P52804	EFNA5_CHICK gallus gall

ALIGNMENTS

RESULT 1
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ID   EFNB3_HUMAN   STANDARD;   PRT;   340 AA.
AC   Q15768; O00680; Q87BH7; Q92875;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ephrin-B3 precursor (EPH-related receptor tyrosine kinase ligand 8)
DE   (LERK-8) (EPH-related receptor transmembrane ligand ELK-L3).
GN   Name=EFNB3; Synonyms=EPLG8, LERK8;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Cerretti D.P.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=97271551; PubMed=9126477; DOI=10.1006/geno.1997.4615;
RA   Tang X.X., Pleasure D.E., Ikegaki N.;
RT   "cDNA cloning, chromosomal localization, and expression pattern of
RT   EPLG8, a new member of the EPLG gene family encoding ligands of EPH-
RT   related protein-tyrosine kinase receptors.";
RL   Genomics 41:17-24(1997).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain cortex;
RX   MEDLINE=96404527; PubMed=8808709;
RA   Gale N.W., Flenniken A., Compton D.C., Jenkins N.A., Copeland N.G.,
RA   Gilbert D.J., Davis S., Wilkinson D.G., Yancopoulos G.D.;
RT   "Elk-L3, a novel transmembrane ligand for the Eph family of receptor
RT   tyrosine kinases, expressed in embryonic floor plate, roof plate and
RT   hindbrain segments.";
RL   Oncogene 13:1343-1352(1996).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

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RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   PROTEIN SEQUENCE OF 28-42.
RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RA   Zhang Z., Henzel W.J.;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
RN   [6]
RX   MEDLINE=99211388; PubMed=10197531; DOI=10.1016/S0896-6273(00)80706-0;
RA   Brueckner K., Pablo Labrador J., Scheffele P., Herb A., Seeburg P.H.,
RA   Klein R.;
RT   "EphrinB ligands recruit GRIP family PDZ adaptor proteins into raft
RT   membrane microdomains.";
RL   Neuron 22:511-524(1999).
CC   -!- FUNCTION: May play a pivotal role in forebrain function. Binds to,
CC       and induce the collapse of, commissural axons/growth cones in
CC       vitro. May play a role in constraining the orientation of
CC       longitudinally projecting axons (By similarity).
CC   -!- SUBUNIT: Interacts with GRIP1 and GRIP2.
CC   -!- INTERACTIONS WITH GRIP1 AND GRIP2.
CC   -!- TISSUE SPECIFICITY: Highly expressed in brain; expressed in
CC       embryonic floor plate, roof plate and hindbrain segments.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE=Fetal brain;
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC   -----------------------------------------------------------------------
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DR   EMBL; U57001; AAB05170.1; -; mRNA.
DR   EMBL; U66406; AAC51203.1; -; mRNA.
DR   EMBL; U62775; AAC50707.1; -; mRNA.
DR   EMBL; BC022499; AAH22499.1; -; mRNA.
DR   EMBL; BC042944; AAH42944.1; -; mRNA.
DR   HSSP; P52800; 1IKO.
DR   Ensembl; ENSG00000108947; Homo sapiens.
DR   HGNC; HGNC:3228; EFNB3.
DR   MIM; 602297; -.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
DR   InterPro; IPR001799; Ephrin.
KW   Developmental protein; Differentiation; Direct protein sequencing;
KW   Glycoprotein; Neurogenesis; Polymorphism; Signal; Transmembrane.
GO;  GO:0005887; C:integral to plasma membrane; TAS.
GO;  GO:0005005; F:transmembrane-ephrin receptor activity; TAS.
GO;  GO:0007267; P:cell-cell signaling; TAS.
GO;  GO:0007399; P:neurogenesis; TAS.
FT   SIGNAL        1     27
FT   CHAIN        28    340       Ephrin-B3.
FT   TOPO_DOM     28    226       Extracellular (Potential).
FT   TRANSMEM    227    247       Potential.
FT   TOPO_DOM    248    340       Cytoplasmic (Potential).
FT   MOTIF       338    340       PDZ recognition motif (Potential).
FT   CARBOHYD    210    210       N-linked (GlcNAc...) (Potential).
FT   DISULFID     62    104       By similarity.
FT   DISULFID     92    156       By similarity.
FT   VARIANT     166    166       R -> Q.
FT                                /FTId=VAR_002356.
SQ   SEQUENCE   340 AA;  35835 MW;  EDEF2A22C2FDE79F CRC64;
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Query Match             100.0%;  Score 1850;  DB 1;  Length 340;
Best Local Similarity   100.0%;
Matches  340;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy    1  MGPPHSGPGGVRVGALLLLGVLVSGLSLEPVVWNSANKRFQAEGGYYLYPQIGDRLDL    60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1  MGPPHSGPGGVRVGALLLLGVLVSGLSLEPVVWNSANKRFQAEGGYYLYPQIGDRLDL    60

Qy   61  LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPANLLLTCDRPDLDLRFTKFQEY   120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPANLLLTCDRPDLDLRFTKFQEY   120

Qy  121  SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP  180

Qy  181  VSEMPEMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  VSEMPEMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL  240

Qy  241  GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG  300

Qy  301  GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYKV  340
         |||||||||||||||||||||||||||||||||||||||
Db  301  GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYKV  340
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RESULT 2
EFNB3_MOUSE

ID   EFNB3_MOUSE    STANDARD;     PRT;   340 AA.
AC   O35393;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ephrin-B3 precursor.
GN   Name=Efnb3;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=98143367; PubMed=9848836; DOI=10.1038/sj.onc.1201557;
RA   Bergemann A.D., Zhang L., Chiang M.-K., Brambilla R., Klein R.,
RA   Flanagan J.G.;
RT   "Ephrin-B3, a ligand for the receptor EphB3, expressed at the midline
RT   of the developing neural tube.";
RL   Oncogene 16:471-480(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
```

```
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [3]
RP   FUNCTION.
RX   MEDLINE=20171264; PubMed=10704386;
RA   Imondi R., Wideman C., Kaprielian Z.;
RT   "Complementary expression of transmembrane ephrins and their receptors
RT   in the mouse spinal cord: a possible role in constraining the
RT   orientation of longitudinally projecting axons.";
RL   Development 127:1397-1410(2000).
CC   -!- FUNCTION: May play a pivotal role in forebrain function. Binds to,
CC       and induce the collapse of, commissural axons/growth cones in
CC       vitro. May play a role in constraining the orientation of
CC       longitudinally projecting axons.
CC   -!- SUBUNIT: Interacts with GRIP1 and GRIP2 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed on lateral floor plate cells,
CC       specifically on commissural axon segments that have passed through
CC       the floor plate. Expressed in cells of the retinal ganglion cell
CC       layer during retinal axon guidance to the optic disk.
CC   -!- DEVELOPMENTAL STAGE: Expressed in the floor plate throughout the
CC       period of commissural axon pathfinding.
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC   -------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -------------------------------------------------------------------------
DR   EMBL; AF025288; AAC53537.1; -; mRNA.
DR   EMBL; BC052001; AAH52001.1; -; mRNA.
DR   EMBL; BC058617; AAH58617.1; -; mRNA.
DR   HSSP; P52800; 1IKO.
DR   Ensembl; ENSMUSG00000003934; Mus musculus.
DR   MGI; MGI:109196; Efnb3.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0007628; P:adult walking behavior; IMP.
DR   GO; GO:0016198; P:axon choice point recognition; IMP.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Differentiation; Glycoprotein; Neurogenesis;
KW   Signal; Transmembrane.
FT   SIGNAL         1     27       Potential.
FT   CHAIN         28    340       Ephrin-B3.
FT   TOPO_DOM      28    227       Extracellular (Potential).
FT   TRANSMEM     228    248       Potential.
FT   TOPO_DOM     249    340       Cytoplasmic (Potential).
FT   MOTIF        338    340       PDZ recognition motif (Potential).
FT   CARBOHYD     210    210       N-linked (GlcNAc...) (Potential).
FT   DISULFID      62    104       By similarity.
FT   DISULFID      92    156       By similarity.
SQ   SEQUENCE   340 AA;  35885 MW;  52F3D58FD209A6B8 CRC64;

Query Match     96.2%;  Score 1780;  DB 1;  Length 340;
Best Local Similarity   95.6%;
Matches  325;  Conservative   7;  Mismatches   8;  Indels   0;  Gaps   0;

Qy    1 MGPPHSGPGGGVRVGALLLLGVLLGVLSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
          ||||| |||||| |||||||| |||||||||||||| |||||| ||||||||||||||||||
Db    1 MGAPHFGPGGGVQVGALLLLGFAGLVSGLSLEPVVWNSANKFQAEGGYVLYPQIGDRLDL 60

Qy   61 LCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
          |||||||||||||| |||||||||| |||| ||||||||||||||||||||||||||||||
Db   61 LCPRARPPGPHSSPSYEFYKLYLVEGAQCRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy  121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy  181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGIALLLL 240
          |||||||||||||| ||| | |||||| ||||||||||||||||||||||||||| |||||
Db  181 VSEMPMERDRGAAHSAEPGRDTIPGDPSSNATSRGAEGPLPPPSMPAVAGAAGGMALLLL 240

Qy  241 GVAGAGGAMCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GVAGAGGAMCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy  301 GAADPPFCPHYEKVSGDYGHRPVYVIVQDGPPSPPNIYYKV 340
          | ||||||||||||||||||| || |||||||||||||||
Db  301 GTADPPFCPHYEKVSGDYGHPVYIVQDGPPSPPNIYYKV 340
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RESULT 3
Q5F221_MOUSE
Q5F221_MOUSE PRELIMINARY;     PRT;    340 AA.
ID   Q5F221;
AC   Q5F221;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Ephrin B3 (16 days embryo head cDNA, RIKEN full-length enriched
DE   library, clone:C130048B01 product:m-ephrin-B3).
GN   Name=Efnb3; ORFNames=RP23-561J20.5-001;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Tromans A.;
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schönbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schönbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
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RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Ohara Y., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanaegaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka Y., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira A., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yaeunishi A., Muramatsu M., Hayashizaki Y.;
DR   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL731687; CAI52012.1; -; Genomic_DNA.
DR   EMBL; AK048305; BAC33299.1; -; mRNA.
SQ   SEQUENCE   340 AA; 35884 MW; 52F3D58FD209A6B8 CRC64;

Qy   1 MGPPHSGPGGVRVGALLLLGVLGVLSVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
            |||||||| | |||||||| ||||||||||||||||||||||||||||||||||||||||||

Db   1 MGPPHSGPGGVRVGALLLLGVLGVLSVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

RESULT 4

Q90231 BRARE

ID   Q90231   BRARE PRELIMINARY;   PRT;   331 AA.
AC   Q90231;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ephrin B3.
GN   Name=efnb3;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21290827; PubMed=11397014; DOI=10.1006/dbio.2001.0281;
RA   Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
RA   Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;
RT   "Morphogenesis of precordial plate and notochord requires intact
RT   eph/ephrin b signaling";
RL   Dev. Biol. 234:470-482(2001).
DR   EMBL; AF375227; AAK64277.1; -; mRNA.
DR   HSSP; P52800; 1IKO.
DR   Ensembl; ENSDARG00000008177; Danio rerio.
DR   ZFIN; ZDB-GENE-010618-3; efnb3.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
DR   PROSITE; PS01299; EPHRIN_1; 1.
SQ   SEQUENCE   331 AA; 35638 MW; 6A5EACD5509A09818 CRC64;

Qy   10 GVRVGALLLLGVLGVLSVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPG 69
            ||||||||||||||||||||||||||||:|:.||||||||||||||||||||:|:||:|||

Db   9 GLGILIFLVDLLG-ITATNMEPIYWNSLNKRFSDDKGYVLYPQIGDRLDLICPSSDPPG   67

Qy   70 PHSSPNYEYKLYLVGG-AQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHE 128
            :|:.||||||||.|.| |.|.||..|||.|||.||:||.||.|.|..|.:.||||||

Db   9 GLGILIFLVDLLG-ITATNMEPIYWNSLNKRFSDDKGYVLYPQIGDRLDLICPSSDPPG   67

DB   9 GLGILIFLVDLLG-ITATNMEPIYWNSLNKRFSDDKGYVLYPQIGDRLDLICPSSDPPG   67

Db   68 PRAPADYEYKLYLVSSREQADRCEVTGAPNLLLTCDKPNSDMRTIKFQEYSPNLWGHE 127

Qy   129 FRSHHDYYIIATSDGTREGLBSLQGGVCLTRGMKVLLRVGQSPRG-GAVPRKPVSEMPME 187
            :|:|||.||||||||||.|:|||||.||.|||||||||||||.| :||.|.|.:||.||

Db   128 FKTNHDYFIIATSDGTRQGLBSMRGGVCA1TQGMKVVLRVGQSPYGLPAKSPKPDS---- 182

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RESULT 5
Q50Q3_BRARE
ID   Q50Q3_BRARE  PRELIMINARY;   PRT;   342 AA.
AC   Q50Q3;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Efnb3 protein.
GN   Name=efnb3;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McKernan P.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RG   NIH MGC Project;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC095605; AAH95605.1; -; mRNA.
SQ   SEQUENCE 342 AA; 36885 MW; 1629532234F85386 CRC64;

Query Match          49.9%;  Score 923;  DB 2;  Length 342;
Best Local Similarity 54.8%;
Matches   190;  Conservative  43;  Mismatches  74;  Indels  40;  Gaps  10;

Qy   10 GVRVGALLLLGVLGVLSLSLLEPVYWNSANKRFQAEGGGYVLYPQIGDRLDLLCPRARPPG  69
          :||  ||| |: ||| ||| |||||||| :||||| :    ||||||||||||||||  ||
Db   20 GLGILLIFLVDLLG-ITATNMEPIYWNSLNKRFSDDKGVVLYPQIGDRLDLICPSSDPG   78

Qy   70 PHSSPNYEPYKLYLVGG-AQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHE  128
          |  : : :|||||||  :  | .|  | ||||||||| |   |||||||||||||||||||
Db   79 PRAPADVEYKLYLVSSREQARDCEVTGAPNLLLTTCDKPNSDMRFTIKFQEYSPNLWGHE  138

Qy  129 FRSHDDYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRG-GAVPRKPVSEMPME  187
          | ::||||||||||||  || | |||||:|||||| ||||||   | |     |  |
Db  139 FKTNHDYFIIATSDGTRQGLESMRGGVCATQGMKVVLKVGQSPYGLPAKSPKPDS-----  193

Qy  188 RDRGAAHSLEPGKENLPGDPTSNAT----------SRGAEGPLPPPSMPAVAGAAGGLAILL  239
                      :| ||  |            ::  |||  ||| |  | ||||||| |.||
Db  183 -----------AGRINNPNPGTGNSTHPQIPPRGSGGENGPLPASNIAVIAGAAGGSAFLL   232

Qy  240 LGVAGAGGAMCWRRRAKPSESRIPGPGSFG------RGGSLGLGGGGGMGPRRAEPGEL   293
          | | :.|  | ||| | :|||  :|||||         ||:|:| |||  | ||::|.|::
Db  233 L-VTAVICVVCYRRHAKHSESHHP-PLSLSLLTSPKRGCGGTGVGGGNNNG---SEPSDI   287

Qy  294 GIALRGGGAADPPPCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV  340
            |: |   .  :::|||||||||||||||:||| .|||||.||||||
Db  288 IIPLR---TSDSAYCPHYEKVSGDYGHPVVIVQEMPPQSPANIYYKV  331
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RESULT 6
Q9PT69_XENLA
ID   Q9PT69_XENLA  PRELIMINARY;   PRT;   327 AA.
AC   Q9PT69;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Ephrin-B3 precursor.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryonic head;
RX   MEDLINE=20099673; PubMed=10633856;
RX   DOI=10.1002/(SICI)1097-0177(199912)216:4/5<361::AID-DVDY5>3.0.CO;2-W;
RA   Helbling P.M., Saulnier D.M.E., Robinson V., Christiansen J.H.,
RA   Wilkinson D.G., Brandli A.W.;
RT   "Comparative analysis of embryonic gene expression defines potential
RT   interaction sites for Xenopus EphB4 receptors with ephrin-B ligands.";
RL   Dev. Dyn. 216:361-373(1999).
RN   [2]
DR   EMBL; AJ236866; CAB65511.1; -; mRNA.
DR   HSSP; P52800; 1IKO.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR002086; Aldehyd_dehydrog.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Signal.
FT   SIGNAL        1     25       Potential.
SQ   SEQUENCE 327 AA; 35913 MW; 4B80FA39D4C22DCD CRC64;

Query Match          49.7%;  Score 919;  DB 2;  Length 327;
Best Local Similarity 60.4%;
Matches   192;  Conservative  30;  Mismatches  82;  Indels  14;  Gaps  8;

Qy   25 VSGLSLEPVYWNSANKRFQAEGGGYVLYPQIGDRLDLLCPRARPGPHSSPNYEPYKLYLV   84
          :| |||:| ||||||||||:: .|||||||||||||||||||  | | ||:||||:|||||
Db   22 ISALSLDPIYWNSANKRFEDTEGYVLYPQIGDRLDLLCPRSEPQGPFSSSPYEYKLYLV    81

Qy   85 GGAQG-RRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDG  143
          | ::  | | : |||||||||||||:||||||||||||:|||||||:| :.|||||||||
Db   82 GTKEEMSSCSILRTPNLLLTCDRPSQDLRFTIKFQEFSPNLWGHEFQSQRDYYIIATSDG  141

Qy  144 TREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPERDRGAAHSL-EPGKEN  202
          | :|:| |||||| |:||||| |:||||: ||  | | ||       |   |: |     
Db  142 TMDGIETLQGGVCETKGMKVTLKVGQSPNGATPPRRPSS---AGKDSGISPSVPNDIPN  198

Qy  203 LPGDPTSNATSRGAEGPLPPPSMPAVAGANAGGLALLLLGVAGAGGAMCWRRRRAKPSESR  262
          :   | ||| | | ||||| | :| |||| .|| |||| :  |.|| | ||||:|| | :|
Db  199 V-GETSGNATKTGENGPLPISHVPLVAGAAGGAALLL-VFGVGWGWVCHRRRQAKHSDTR  256

Qy  263 HPGPGSFGRGGSLGLGGGGGMGPRRAEPGELGIALRGGGAADPPPCPHYEKVSGDYGHPV  322
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Db  188 RDRGAAHSLEPGKENLPGDPTSNAT----------SRGAEGPLPPPSMPAVAGAAGGLAILL  239
Db  194 -----------AGRINNPNPGTGNSTHPQIPPRGSGGENGPLPASNIAVIAGAAGGSAFL    243
Db  240 LGVAGAGGAMCWRRRAKPSESRIPGPGSFG------RGGSLGLGGGGGMGPRRAEPGEL    293
Db  244 L-VTAVICVVCYRRHAKHSESHHP-PLSLSLLTSPKRGCGGTGVGGGNNNG---SEPSDI   298
Db  294 GIALRGGGAADPPPCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV  340
Db  299 IIPLR---TSDSAYCPHYEKVSGDYGHPVVIVQEMPPQSPANIYYKV  342
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Db     257  HP-PLSLGSITSPKRGGNN-----NGHEPSDIIMPLRPSEAG--AFCPHYEKVSGDYGHPV 309
              ||||  | :: ||     | :: || ||||||||||||||||
Qy     323  YIVQDGPGPSPNIYYKV 340
              ||||| |||||| |||||
Db     310  YIVQDMASQSPANIYYKV 327
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RESULT 7
EFNB2_MOUSE
ID    EFNB2_MOUSE        STANDARD;      PRT;    336 AA.
AC    P52800;
DT    01-OCT-1996 (Rel. 34, Created)
DT    01-OCT-1996 (Rel. 34, Last sequence update)
DT    10-MAY-2005 (Rel. 47, Last annotation update)
DE    Ephrin-B2 precursor (EPH-related receptor tyrosine kinase ligand 5)
DE    (LERK-5) (HTK ligand) (HTK-L) (ELF-2).
GN    Name=Efnb2; Synonyms=Elf2, Epl5, Epl95, Htkl, Lerk5;
OS    Mus musculus (Mouse).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC    Muroidea; Muridae; Murinae; Mus.
OX    NCBI_TaxID=10090;
RN    [1]
RP    NUCLEOTIDE SEQUENCE.
RX    MEDLINE=96145238; PubMed=8559144; DOI=10.1016/0161-5890(95)00108-5;
RA    Cerretti D.P., Vanden Bos T., Nelson N., Kozlosky C.J., Reddy P.,
RA    Maraskovsky E., Park L.S., Lyman S.D., Copeland N.G., Gilbert D.J.,
RA    Jenkins N.A., Fletcher R.A.,
RT    "Isolation of LERK-5: a ligand of the eph-related receptor tyrosine
RT    kinases.";
RL    Mol. Immunol. 32:1197-1205(1995).
RN    [2]
RP    NUCLEOTIDE SEQUENCE.
RX    MEDLINE=95199254; PubMed=7534404;
RA    Bennett B.D., Zeigler F.C., Gu Q., Fendly B., Goddard A.D.,
RA    Gillett N., Matthews W.,
RT    "Molecular cloning of a ligand for the EPH-related receptor protein-
RT    tyrosine kinase Htk.";
RL    Proc. Natl. Acad. Sci. U.S.A. 92:1866-1870(1995).
RN    [3]
RP    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC    STRAIN=ICR; TISSUE=Brain;
RX    MEDLINE=95379837; PubMed=7651410;
RA    Bergemann A.D., Cheng H.J., Brambilla R., Klein R., Flanagan J.G.;
RT    "ELF-2, a new member of the Eph ligand family, is segmentally
RT    expressed in mouse embryos in the region of the hindbrain and newly
RT    forming somites.";
RL    Mol. Cell. Biol. 15:4921-4929(1995).
RN    [4]
RP    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC    STRAIN=C57BL/6J; TISSUE=Brain;
RX    MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA    Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA    Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA    Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA    Hopkins R.F., Jordan H.F., Moore T., Max S.I., Wang J., Hsieh F.,
RA    Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA    Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA    Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA    Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA    Bosak S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA    Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA    Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA    Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA    Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA    Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA    Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA    Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA    Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT    "Generation and initial analysis of more than 15,000 full-length human
RT    and mouse cDNA sequences.";
RL    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN    [5]
RP    FUNCTION.
RX    MEDLINE=20171264; PubMed=10704386;
RA    Imondi R., Wideman C., Kaprielian Z.;
RT    "Complementary expression of transmembrane ephrins and their receptors
RT    in the mouse spinal cord: a possible role in constraining the
RT    orientation of longitudinally projecting axons.";
RL    Development 127:1397-1410(2000).
RN    [6]
RP    X-RAY CRYSTALLOGRAPHY (1.92 ANGSTROMS) OF 30-170.
RX    PubMed=11709926; DOI=10.1016/S1534-5807(01)00002-8;
RA    Toch J., Cutforth T., Gelinas A.D., Bethoney K.A., Bard J.,
RA    Harrison C.J.;
RT    "Crystal structure of an ephrin ectodomain.";
RL    Dev. Cell 1:83-92(2001).
RN    [7]
RP    X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 31-168 IN COMPLEX WITH EPHB2.
RX    PubMed=11780069; DOI=10.1038/414933a;
RA    Himanen J.-P., Rajashankar K.R., Lackmann M., Cowan C.A.,
RA    Henkemeyer M., Nikolov D.B.;
RT    "Crystal structure of an Eph receptor-ephrin complex.";
RL    Nature 414:933-938(2001).
CC   -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB2 and EPHB4.
CC        May play a role in constraining the orientation of longitudinally
CC        projecting axons.
CC   -!- SUBUNIT: Interacts with PDZRN3 (By similarity). Binds to the
CC        receptor tyrosine kinase EPHB4.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed on lateral floor plate cells,
CC        specifically on commissural axon segments that have passed through
CC        the floor plate. Expressed in cells of the retinal ganglion cell
CC        layer during retinal axon guidance to the optic disk.
CC   -!- DEVELOPMENTAL STAGE: Expressed in the floor plate throughout the
CC        period of commissural axon pathfinding.
CC   -!- PTM: Inducible phosphorylation of tyrosine residues in the
CC        cytoplasmic domain (By similarity).
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC   --------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --------------------------------------------------------------------------
DR   EMBL; U16819; AAA99708.1; -; mRNA.
DR   EMBL; L38847; AAC42052.1; -; mRNA.
DR   EMBL; U30244; AAA82934.1; -; mRNA.
DR   EMBL; BC057009; AAH57009.1; -; mRNA.
PIR; I49766; I49766.
PDB; 1KGY; X-ray; E/F/G/H=31-168.
PDB; 1IKO; X-ray; P=30-207.
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; Ephrin.
PRINTS; PR01347; Ephrin.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
MGI; MGI:105097; Efnb2.
Ensembl; ENSMUSG00000001300; Mus musculus.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0005886; C:plasma membrane; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0001945; P:lymph vessel development; IMP.
GO; GO:0009887; P:organogenesis; IMP.
KW   3D-structure; Developmental protein; Differentiation; Glycoprotein;
KW   Neurogenesis; Phosphorylation; Signal; Transmembrane.
FT   SIGNAL        1     28       Potential.
FT   CHAIN        29    336       Ephrin-B2.
FT   TOPO_DOM     29    232       Extracellular (Potential).
FT   TRANSMEM    233    253       Potential.
FT   TOPO_DOM    254    336       Cytoplasmic (Potential).
FT   MOTIF       334    336       PDZ recognition motif (Potential).
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FT   CARBOHYD     39     39       N-linked (GlcNAc...).
FT   CARBOHYD    142    142       N-linked (GlcNAc...).
FT   DISULFID     65    104
FT   DISULFID     92    156
FT   CONFLICT    177    177       Missing (in Ref. 3).
FT   CONFLICT      3      4       A -> T (in Ref. 1).
FT   STRAND       36     37
FT   TURN         40     41
FT   STRAND       43     44
FT   STRAND       46     46
FT   TURN         47     49
FT   STRAND       50     52
FT   STRAND       57     58
FT   TURN         60     65
FT   TURN         72     73
FT   STRAND       79     84
FT   HELIX        86     90
FT   HELIX        91     92
FT   TURN         93     93
FT   STRAND       99    104
FT   STRAND      107    108
FT   STRAND      111    116
FT   STRAND      124    125
FT   STRAND      131    132
FT   TURN        134    139
FT   HELIX       145    147
FT   TURN        148    149
FT   STRAND      152    152
FT   TURN        152    154
FT   STRAND      154    154
FT   HELIX       155    158
FT   TURN        162    166
SQ   SEQUENCE    336 AA;  37202 MW;  D08949996E399554 CRC64;
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RESULT 8

Query Match 34.5%; Score 637.5; DB 1; Length 336;
Best Local Similarity 42.1%; Pred. No. 3.5e-33;
Matches 139; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

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Qy   14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQABGGYVLLYPQIGDRLDLLCPRARPGGHSS  73
         | : :|| :|:| ||||| ||||| .|. || |:||||||| ||: ||
Db   17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGGQLVLYPQIGDKLDIICPKV---DSKTV  73

Qy   74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
         | |:|| :|:| || || |  | |: :||| | |: :||||||||.|||||||:|| .:
Db   74 GQYEYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK  133

Qy  134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
         |||| :||:| ||| . :.|||| || |:|:|||   ::.|:| :   |  || | : |
Db  134 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

Qy  191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGGAGAMC 250
         | :: ..  |:| |  |:. .| | :|  |   :   |||:.| : :::: |: || |
Db  194 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIFIVIIILVVLLL   253

Qy  251 WRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH   310
          ||:: :    |  :   :    .  .   | ::.|    :  :  ||::   | ||
Db  254 KYRRHRHKHSPQHTTTLSLSTLATPKRGGNN---NGSEPSDVIIPLR---TADSVFCPH  306

Qy  311 YEKVSGDYGHPVIVQDGPPQSPPNIYYKV 340
         |||||||||||||| . |||||.||||||
Db  307 YEKVSGDYGHPVIVQEMPPQSPANIYYKV  336
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ID   Q4FJM3_MOUSE   PRELIMINARY;   PRT;   336 AA.
AC   Q4FJM3;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Efnb2 protein.
GN   Name=Efnb2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Ebert L., Muenstermann E., Schatten R., Henze S., Bohn E.,
RA   Mollenhauer J., Wiemann S., Schick M., Korn B.;
RT   "Cloning of mouse full open reading frames in Gateway(R) system entry
RT   vector (pDONR201).";
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CT010381; CAJ18588.1; -; mRNA.
SQ   SEQUENCE   336 AA; 37202 MW; D08949996E399554 CRC64;

RESULT 9

Query Match 34.5%; Score 637.5; DB 2; Length 336;
Best Local Similarity 42.1%; Pred. No. 3.5e-33;
Matches 139; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

```
Qy   14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQABGGYVLLYPQIGDRLDLLCPRARPGGHSS  73
         | : :|| :|:| ||||| ||||| .|. || |:||||||| ||: ||
Db   17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGGQLVLYPQIGDKLDIICPKV---DSKTV  73

Qy   74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
         | |:|| :|:| || || |  | |: :||| | |: :||||||||.|||||||:|| .:
Db   74 GQYEYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK  133

Qy  134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
         |||| :||:| ||| . :.|||| || |:|:|||   ::.|:| :   |  || | : |
Db  134 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

Qy  191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGGAGAMC 250
         | :: ..  |:| |  |:. .| | :|  |   :   |||:.| : :::: |: || |
Db  194 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIFIVIIILVVLLL   253

Qy  251 WRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH   310
          ||:: :    |  :   :    .  .   | ::.|    :  :  ||::   | ||
Db  254 KYRRHRHKHSPQHTTTLSLSTLATPKRGGNN---NGSEPSDVIIPLR---TADSVFCPH  306

Qy  311 YEKVSGDYGHPVIVQDGPPQSPPNIYYKV 340
         |||||||||||||| . |||||.||||||
Db  307 YEKVSGDYGHPVIVQEMPPQSPANIYYKV  336
```

ID   EFNB1_HUMAN   STANDARD;   PRT;   346 AA.
AC   P98172;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Ephrin-B1 precursor (EPH-related receptor tyrosine kinase ligand 2)
DE   (LERK-2) (ELK ligand) (ELK-L).
GN   Name=EFNB1; Synonyms=EPL-3, EPLG2, LERK2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=94349923; PubMed=8070404;
RA   Beckmann M.P., Cerretti D.P., Baum P., Vanden Bos T., James L.,
RA   Farrah T., Kozlosky C., Hollingsworth T., Shilling H., Maraskovsky E.,
RA   Fletcher F.A., Lhotak V., Pawson T., Lyman S.D.;
RT   "Molecular characterization of a family of ligands for eph-related
RT   tyrosine kinase receptors.";
RL   EMBO J. 13:3757-3762(1994).
RC   TISSUE=Placenta;
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=95069919; PubMed=7973638;
RA   Davis S., Gale N.W., Aldrich T.H., Maisonpierre P.C., Lhotak V.,
RA   Pawson T., Goldfarb M., Yancopoulos G.D.;
RT   "Ligands for EPH-related receptor tyrosine kinases that require

RT   membrane attachment or clustering for activity.";
RL   Science 266:816-819(1994).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Fletcher F.A., Huebner K., Shaffer L.G., Monaco A., Mueller U.,
RA   Kozlosky C., Druck T., Simoneaux D.K., Fairweather N., Chelly J.,
RA   Cerretti D.P., Belmont J.W., Beckmann M.P., Lyman S.D.;
RT   "Assignment of the human Elk ligand gene, EPLG2, to chromosome region
RT   Xq12.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15772651; DOI=10.1038/nature03440;
RA   Ross M.T., Grafham D.V., Coffey A.J., Scherer S., McLay K., Muzny D.,
RA   Platzer M., Howell G.R., Burrows C., Bird C.P., Frankish A.,
RA   Lovell F.L., Howe K.L., Ashurst J.L., Fulton R.S., Sudbrak R., Wen G.,
RA   Jones M.C., Hurles M.E., Andrews T.D., Scott C.E., Searle S.,
RA   Ramser J., Whittaker A., Deadman R., Carter N.P., Hunt S.E., Chen R.,
RA   Cree A., Gunaratne P., Havlak P., Hodgson A., Metzker M.L.,
RA   Richards S., Scott G., Steffen D., Sodergren E., Wheeler D.A.,
RA   Worley K.C., Ainscough R., Ambrose K.D., Ansari-Lari M.A., Aradhya S.,
RA   Ashwell R.I., Babbage A.K., Bagguley C.L., Ballabio A., Banerjee R.,
RA   Barker G.E., Barlow K.F., Barrett I.P., Bates K.N., Beare D.M.,
RA   Beasley H., Beasley O., Beck A., Bethel G., Blechschmidt K., Brady N.,
RA   Bray-Allen S., Bridgeman A.M., Brown A.J., Brown M.J., Bonnin D.,
RA   Bruford E.A., Buhay C., Burch P., Burford D., Burgess J., Burrill W.,
RA   Burton J., Bye J.M., Carder C., Carrel L., Chako J., Chapman J.C.,
RA   Chavez D., Chen E., Chen G., Chen Y., Chen Z., Chinault C.,
RA   Ciccodicola A., Clark S.Y., Clarke G., Clee C.M., Clegg S.,
RA   Clerc-Blankenburg K., Clifford K., Cobley V., Cole C.G., Conquer J.S.,
RA   Corby N., Connor R.E., David R., Davies J., Davis C., Davis J.,
RA   Delgado O., Deshazo D., Dhami P., Ding Y., Dinh H., Dodsworth S.,
RA   Draper H., Dugan-Rocha S., Dunham A., Dunn M., Durbin K.J., Dutta I.,
RA   Eades T., Ellwood M., Emery-Cohen A., Errington H., Evans K.L.,
RA   Faulkner L., Francis F., Frankland J., Fraser A.E., Galgoczy P.,
RA   Gilbert J., Gill R., Gloeckner G., Gregory S.G., Gribble S.,
RA   Griffiths C., Grocock R., Gu Y., Gwilliam R., Hamilton C., Hart E.A.,
RA   Hawes A., Heath P.D., Heitmann K., Hennig S., Hernandez J.,
RA   Hinzmann B., Ho S., Hoffs M., Howden P.J., Huckle E.J., Hume J.,
RA   Hunt P.J., Hunt A.R., Isherwood J., Jacob L., Johnson D., Jones S.,
RA   de Jong P.J., Joseph S.S., Keenan S., Kelly S., Kershaw J.K., Khan Z.,
RA   Kioschis P., Klages S., Knights A.J., Kosiura A., Kovar-Smith C.,
RA   Laird G.K., Langford C., Lawlor S., Leversha M., Lewis L., Liu W.,
RA   Lloyd C., Lloyd D.M., Loulseged H., Loveland J.E., Lovell J.D.,
RA   Lozado R., Lu J., Lyne R., Ma J., Maheshwari M., Matthews L.H.,
RA   McDowall J., McLaren S., McMurray A., Meidl P., Meitinger T.,
RA   Milne S., Miner G., Mistry S.L., Morgan M., Morris S., Mueller I.,
RA   Mullikin J.C., Nguyen N., Nordsiek G., Nyakatura G., O'dell C.N.,
RA   Okwuonu G., Palmer S., Pandian R., Parker D., Parrish J.,
RA   Pasternak S., Patel D., Pearce A.V., Pearson D.M., Pelan S.E.,
RA   Perez L., Porter K.M., Ramsey Y., Reichwald K., Rhodes S.,
RA   Ridler K.A., Schlessinger D., Schueler M.G., Sehra H.K.,
RA   Shaw-Smith C., Shen H., Sheridan E.M., Shownkeen R., Skuce C.D.,
RA   Smith M.L., Sotheran E.C., Steingruber H.E., Steward C.A., Storey R.,
RA   Swann R.M., Swarbreck D., Tabor P.E., Taudien S., Taylor T.,
RA   Teague B., Thomas K., Thorpe A., Timms K., Tracey A., Trevanion S.,
RA   Tromans A.C., d'Urso M., Verduzco D., Villasana D., Waldron L.,
RA   Wall M., Wang Q., Warren J., Warry G.L., Wei X., West A.,
RA   Whitehead S.L., Whiteley M.N., Wilkinson J.E., Willey D.L.,
RA   Williams G., Williams L., Williamson A., Williamson H., Wilming L.,
RA   Woodmansey R.L., Wray P.W., Yen J., Zhang J., Zhou J., Zoghbi H.,
RA   Zorilla S., Buck D., Reinhardt R., Poustka A., Rosenthal A.,
RA   Lehrach H., Meindl A., Minx P.J., Hillier L.W., Willard H.F.,
RA   Nelson D.L., Weinstock G., Sulston J.E., Durbin R., Hubbard T.,
RA   Gibbs R.A., Beck S., Rogers J., Bentley D.R.;
RT   "The DNA sequence of the human X chromosome.";
RL   Nature 434:325-337(2005).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Eye, and Skin;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   PROTEIN SEQUENCE OF 28-42.
RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RA   Zhang Z., Henzel W.J.;
RT   "signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
RN   [7]
RP   INTERACTIONS WITH GRIP1 AND GRIP2.
RC   TISSUE=Fetal brain;
RX   MEDLINE=99211388; PubMed=10197531; DOI=10.1016/S0896-6273(00)80706-0;
RA   Brueckner K., Pablo Labrador J., Scheffele P., Herb A., Seeburg P.H.,
RA   Klein R.;
RT   "EphrinB ligands recruit GRIP family PDZ adaptor proteins into raft
RT   membrane microdomains.";
RL   Neuron 22:511-524(1999).
RN   [8]
RP   VARIANTS CFNS LEU-54 AND ILE-111.
RX   PubMed=15124102; DOI=10.1086/421532;
RA   Wieland I., Jakubiczka S., Muschke P., Cohen M., Thiele H.,
RA   Gerlach K.L., Adams R.H., Wieacker P.;
RT   "Mutations of the ephrin-B1 gene cause craniofrontonasal syndrome.";
RL   Am. J. Hum. Genet. 74:1209-1215(2004).
RN   [9]
RP   VARIANTS CFNS THR-62; SER-98; PRO-115; HIS-119; THR-119; SER-151;
RP   VAL-151; PRO-155; ILE-158 AND VAL-158, AND VARIANT HIS-154.
RX   PubMed=15166289; DOI=10.1073/pnas.0402819101;
RA   Twigg S.R.F., Kan R., Babbs C., Bochukova E.G., Robertson S.P.,
RA   Wall S.A., Morriss-Kay G.M., Wilkie A.O.M.;
RT   "Mutations of ephrin-B1 (EFNB1), a marker of tissue boundary
RT   formation, cause craniofrontonasal syndrome.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:8652-8657(2004).
RN   [10]
RP   VARIANTS CFNS ARG-27; LEU-54; SER-119; HIS-119; ALA-137; PHE-138;
RP   SER-151; SER-153; TYR-153 AND ARG-182.
RX   PubMed=15959873; DOI=10.1002/humu.20193;
RA   Wieland I., Reardon W., Jakubiczka S., Franco B., Kress W.,
RA   Vincent-Delorme C., Thierry P., Edwards M., Koenig R., Rusu C.,
RA   Schweiger S., Thompson E., Tinschert S., Stewart F., Wieacker P.;
RT   "Twenty-six novel EFNB1 mutations in familial and sporadic
RT   craniofrontonasal syndrome (CFNS).";
RL   Hum. Mutat. 26:1-6(2005).
CC   -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB1 and EPHA1.
CC   Binds to, and induce the collapse of, commissural axons/growth
CC   cones in vitro. May play a role in constraining the orientation of
CC   longitudinally projecting axons (By similarity).
CC   -!- SUBUNIT: Interacts with GRIP1 and GRIP2.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Heart, placenta, lung, liver, skeletal muscle,
CC   kidney, pancreas.
CC   -!- INDUCTION: By TNF-alpha.
CC   -!- PTM: Inducible phosphorylation of tyrosine residues in the
CC   cytoplasmic domain (By similarity).
CC   -!- DISEASE: Defects in EFNB1 are a cause of craniofrontonasal

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CC   syndrome (CFNS) [MIM:304110]; also known as craniofrontonasal
CC   dysplasia (CFND). CFNS is an X-linked inherited syndrome
CC   characterized by hypertelorism, coronal synostosis with
CC   brachycephaly, downslanting palpebral fissures, clefting of the
CC   nasal tip, joint anomalies, longitudinally grooved fingernails and
CC   other digital anomalies.
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC
```

```
DR   EMBL; U09304; AAA53093.1; -; mRNA.
DR   EMBL; L37361; AAA52369.1; -; mRNA.
DR   EMBL; U09303; AAB41127.1; -; mRNA.
DR   EMBL; AL136092; CAB86409.1; -; Genomic_DNA.
DR   EMBL; BC016649; AAH16649.1; -; mRNA.
DR   EMBL; BC052979; AAH52979.1; -; mRNA.
DR   PIR; S46993; S46993.
DR   HSSP; P52800; 1IKO.
DR   HGNC; HGNC:3226; EFNB1.
DR   Ensembl; ENSG00000090776; Homo sapiens.
DR   H-InvDB; HIX0016846; -.
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Query Match       34.2%;    Score 632;   DB 1;   Length 346;
Best Local Similarity   39.5%;    Pred. No. 8.2e-33;
Matches 145;   Conservative 48;   Mismatches 116;   Indels 58;   Gaps 9;

Qy     8 PGGVRVGALLLLGVILGLVSGL------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
           |:||:| |:|  |  | |:||        :||| | || |:| || | |  | ::||  ||
Db     4 PGGRWLGKWLVAMVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy    62 CPRARPPGPHSSPNYEFVKLYLYVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKPQEYS 121
           |::|| |||     |:||||| | :|    ||   |  ||:| |:|| :| |||||||:|
Db    64 CPRAEAGRP-----YEYVKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKPQEFS 118

Qy   122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
           ||:.|:EF::HHDYYI :||:| :EGLE:L:GGVC TR MK::::VGQ:P  . VP:: :
Db   119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy   182 SEMPMERDRGAAHSLE-PGKENLPGDPTPSNATSRGAGPLPPPSMPAVAGAGGLA----- 236
           S :. |:: .. :  : PG:: .    :   ::::. :   .          ::|
Db   179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP------GASCGGSSGDPD 231

Qy   237 ------LLILGVAGAGGA------MCWRRRAKPSESRHPGPGSFGRGGSLGL 277
                 |::| :|||  .      :  |||   |::   :|   | |::|:|
Db   232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKURKHRKHTQQ------RAAALSL 282

Qy   278 ----GGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHFVYIVQDGPPQSP 333
                  | | :  |   |  |:|  | ::   ||:|||||||||||||||||:: |||||
Db   283 STLASPKGGSGTAGTEFSDIIIPLR--TTENNYCPHYEKVSGDYGHFVYIVQEMPPQSP 339

Qy   334 PNIYYKV 340
           .||||||
Db   340 ANIYYKV 346
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RESULT 10
ID   EFNB2_HUMAN    STANDARD;    PRT;   333 AA.
AC   P52799;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ephrin-B2 precursor (EPH-related receptor tyrosine kinase ligand 5)
DE   (LERK-5) (HTK ligand) (HTK-L).
GN   Name=EFNB2; Synonyms=EPLG5, HTKL, LERK5;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
```

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OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=96145238; PubMed=8559144; DOI=10.1016/0161-5890(95)00108-5;
RA   Cerretti D.P., Vanden Bos T., Nelson N., Kozlosky C.J., Reddy P.,
RA   Maraskovsky E., Park L.S., Lyman S.D., Copeland N.G., Gilbert D.J.,
RA   Jenkins N.A., Fletcher R.A.;
RT   "Isolation of LERK-5: a ligand of the eph-related receptor tyrosine
RT   kinases.";
RL   Mol. Immunol. 32:1197-1205(1995).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=95199254; PubMed=7534404;
RA   Bennett B.D., Zeigler F.C., Gu Q., Fendly B., Goddard A.D.,
RA   Gillett N., Matthews W.;
RT   "Molecular cloning of a ligand for the EPH-related receptor protein-
RT   tyrosine kinase Htk.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:1866-1870(1995).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=98192220; PubMed=9533549;
RA   Vogt T., Stolz W., Welsh J., Jung B., Kerbel R.S., Kobayashi H.,
RA   Landthaler M., McClelland M.;
RT   "Overexpression of Lerk-5/Eplg5 messenger RNA; a novel marker for
RT   increased tumorigenicity and metastatic potential in human malignant
RT   melanomas.";
RL   Clin. Cancer Res. 4:791-797(1998).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB4 and EPHA3.
CC       May play a role in constraining the orientation of longitudinally
CC       projecting axons (By similarity).
CC   -!- SUBUNIT: Interacts with PDZRN3 (By similarity). Binds to the
CC       receptor tyrosine kinases EPHB4 and EPHA3.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Lung and kidney.
CC   -!- PTM: Inducible phosphorylation of tyrosine residues in the
CC       cytoplasmic domain (By similarity).
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC
```

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DR   EMBL; U16797; AAA99707.1; -; mRNA.
DR   EMBL; L38734; AAC41752.1; -; mRNA.
DR   EMBL; U81262; AAD03786.1; -; mRNA.
```

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RESULT 11

Q5JV56_HUMAN
ID   Q5JV56_HUMAN PRELIMINARY;       PRT;   333 AA.
AC   Q5JV56;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Ephrin-B2 (Fragment).
GN   Name=EFNB2; ORFNames=RP11-272L14.1-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

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OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Dunn M.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL138689; CAI39907.1; -; Genomic_DNA.
DR   GO; GO:0016020; C:membrane; IEA.
FT   NON_TER   333    333
SQ   SEQUENCE   333 AA;  36923 MW;  6D9932A632626AEA CRC64;
```

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DR   EMBL; BC069342; AAH69342.1; -; mRNA.
DR   EMBL; BC074856; AAH74856.1; -; mRNA.
DR   EMBL; BC074857; AAH74857.1; -; mRNA.
DR   PIR; I84743; I84743.
DR   SMR; P52800; 1IKO.
DR   HSSP; P52800; 1IKO.
DR   PIR; P52799; 27-167.
DR   Ensembl; ENSG00000125266; Homo sapiens.
DR   HGNC; HGNC:3227; EFNB2.
DR   MIM; 600527; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005886; C:plasma membrane; TAS.
DR   GO; GO:0048875; F:ephrin receptor binding; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0009653; P:morphogenesis; TAS.
KW   Developmental protein; Differentiation; Glycoprotein; Neurogenesis;
KW   Phosphorylation; Signal; Transmembrane.
DR   Interpro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
FT   SIGNAL      1     27
FT   CHAIN      28    333   Ephrin-B2.
FT   TOPO_DOM   28    229   Extracellular (Potential).
FT   TRANSMEM  230    250   Potential.
FT   TOPO_DOM  251    333   Cytoplasmic (Potential).
FT   MOTIF     331    333   PDZ recognition motif (Potential).
FT   CARBOHYD   36     36   N-linked (GlcNAc...) (Potential).
FT   CARBOHYD  139    139   N-linked (GlcNAc...) (Potential).
FT   DISULFID   62    101   By similarity.
FT   DISULFID   89    153   By similarity.
SQ   SEQUENCE   333 AA;  36923 MW;  6D9932A632626AEA CRC64;

Query Match             34.0%;  Score 629.5;  DB 1;  Length 333;
Best Local Similarity   40.9%;  Pred. No. 1.1e-32;
Matches  135;  Conservative  52;  Mismatches  130;  Indels  13;  Gaps  5;

Qy    14 GALLLLGVLGLVSGLSLEPVYWNSANKRPQAEGGYVLYPQIGDRLDLLCPRARPPGHSS 73
            |:|:| ||||||:|||:||:||:||||||||||: :|||:  ||:||:||::  :|:
Db    14 GVLMVLCRTAISKSIVLEPIYWNSNSNSKFLPGGQLVLYPQIGDKLDIICPKV---DSKTV 70

Qy    74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
            |:  |||  |||||||||||||| ||| | ||:|  |||:||:|||||||||:||| |
Db    71 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy   134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPER-DR 190
            ||||:||||||||||||||||||:||||||||||:|    || |||:|||||||| ||
Db   131 DYYIISTNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy   191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVGAAGGLALLLLGVAGAGAMC 250
            |||||||||||||||||||||||||  |||||||||||||||||||||||:||||||:
Db   191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCCIIFIVIITLVLLL 250

Qy   251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
            ||||| |||||: :| |||  |||||:|||||||||| |||||:|||:|||  |||:|||
Db   251 KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSSPSDIIIPLR---TADSVFCPH 303

Qy   311 YEKVSGDYGHPVVIVQDGPPQSPPNIYYKV 340
            ||||||||||||||||| |||||| |||||
Db   304 YEKVSGDYGHPVVIVQEMPPQSPANIYYKV 333
```

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RESULT 12

Q9PUJ4_CHICK
ID   Q9PUJ4_CHICK PRELIMINARY;       PRT;   333 AA.
AC   Q9PUJ4;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ephrin-B2 precursor.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Menzel P., Pasquale E.B.;
RT   "Coding sequence of chicken ephrin-B2.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF180729; AAD53948.1; -; mRNA.
DR   HSSP; P52800; 1IKO.
DR   SMR; Q9PUJ4; 29-169.
DR   Ensembl; ENSGALG00000016856; Gallus gallus.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Signal.
FT   SIGNAL      1     27   Potential.
FT   CHAIN      28    333   ephrin-B2.
SQ   SEQUENCE   333 AA;  36761 MW;  4C28E8CB211B7783 CRC64;

Query Match             34.0%;  Score 629.5;  DB 2;  Length 333;
Best Local Similarity   40.9%;  Pred. No. 1.1e-32;
Matches  135;  Conservative  52;  Mismatches  130;  Indels  13;  Gaps  5;

Qy    14 GALLLLGVLGLVSGLSLEPVYWNSANKRPQAEGGYVLYPQIGDRLDLLCPRARPPGHSS 73
            |:|:| ||||||:|||:||:||:||||||||||: :|||:  ||:||:||::  :|:
Db    14 GVLMVLCRTAISKSIVLEPIYWNSNSNSKFLPGGQLVLYPQIGDKLDIICPKV---DSKTV 70

Qy    74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
            |:  |||  |||||||||||||| ||| | ||:|  |||:||:|||||||||:||| |
Db    71 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy   134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPER-DR 190
            ||||:||||||||||||||||||:||||||||||:|    || |||:|||||||| ||
Db   131 DYYIISTNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy   191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVGAAGGLALLLLGVAGAGAMC 250
            |||||||||||||||||||||||||  |||||||||||||||||||||||:||||||:
Db   191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCCIIFIVIITLVLLL 250

Qy   251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
            ||||| |||||: :| |||  |||||:|||||||||| |||||:|||:|||  |||:|||
Db   251 KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSSPSDIIIPLR---TADSVFCPH 303

Qy   311 YEKVSGDYGHPVVIVQDGPPQSPPNIYYKV 340
            ||||||||||||||||| |||||| |||||
Db   304 YEKVSGDYGHPVVIVQEMPPQSPANIYYKV 333
```

RESULT 13

```
Qy    Query Match    34.0%;  Score 629.5;  DB 2;  Length 333;
      Best Local Similarity   40.5%;  Pred No. 1.1e-32;
      Matches  135;  Conservative  52;  Mismatches 125;  Indels  21;  Gaps   6;

Qy     14  GALILLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVYLYPQIGDRLLDLLCPRARPPGHSS  73
               ||:||:|.||| ||.|:.||:.::||.|:  |:.||| :||| |:||:::|  ||.|:|
Db     16  GALMVLWRTALAKSIVLDPIYWNSSNPKFLPGQOLVLYPQIGDKLDIICPKV---DSKTV  72

Qy     74  PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH  133
               |||:|.| ||| |.||:||:|::||:|||||||:||:|||||||:||.||| |||:||
Db     73  GQYEYKVYMVDKDQADSCAIRKDNTPLLNCAKPDQDVKPTIKFQEFSPNLWGLBFQXNK  132

Qy    134  DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMER----  188
               |:||:|::||.|||||:.||||||.||||||||||:|.||||.||:||:||  |
Db    133  DYYVISTSNGSLEGLNNQGBGVVCQTKTMKILMKVGQDPNSAGLPR---STDPTKRPEQEA  189

Qy    189  -DRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALILLLGVAGAGG  247
               :||:.||:|||.:||| |||:|:.|||. :.|||.|. |: || |||||||:|.||.
Db    190  GTNGKSSTTSPVKDHSGSSTDG--SKAGHSSIIGSEVALFAGIASGCIFIVIIIILVV  247

Qy    248  AMCWRRRRAKPSESRHPGPGSFGRGGSILGLGGGGGMGPREAEPGELGIALRGGGAADPF  307
               :|.||||:|:||.|.|||.|.|||||.:.|:||||||||:|.||| |.|||..||.||
Db    248  LLLKYRRHRHKHSPQHTTTLSLSTLATEPKRSGNN----NGSEPSDIIIPLR---TADSVF  300

Qy    308  CPHYEKVSGDYGHPVYIVQDGPPQOSPNIYYKV  340
               ||||||||||||||||||||||:|||:||||||
Db    301  CPHYEKVSGDYGHPVYIVQEMPPQSPANIYYKV  333
```

EFNB1_CHICK

```
ID   EFNB1_CHICK     STANDARD;      PRT;    334 AA.
AC   O73612;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ephrin-B1 precursor (CEK5 ligand) (CEL5-L).
GN   Name=EFNB1;
OS   Gallus gallus (chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=97223524; PubMed=9070326; DOI=10.1006/dbio.1996.8496;
RA   Holash J.A., Soans C., Chong L.D., Shao H., Dixit V.M., Pasquale E.B.;
RT   "Reciprocal expression of the Eph receptor Cek5 and its ligand(s) in
RT   the early retina.";
RL   Dev. Biol. 182:256-269(1997).
CC   -!- SUBUNIT: Binds to the receptor tyrosine kinase EPHB2. Interacts
CC       with GRIP1 and GRIP2 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: Inducible phosphorylation of tyrosine residues in the
CC       cytoplasmic domain (By similarity).
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC   --------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --------------------------------------------------------------------------
DR   EMBL; U72394; AAC07986.1; -; mRNA.
DR   HSSP; P52800; 1IKO.
DR   Pfam; PF00812; Ephrin; 1.
DR   InterPro; IPR001799; Ephrin.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Differentiation; Glycoprotein; Neurogenesis;
KW   Phosphorylation; Signal; Transmembrane.
FT   SIGNAL        1     25
FT   CHAIN        26    334       Ephrin-B1.
FT   TOPO_DOM     26    231       Extracellular (Potential).
FT   TRANSMEM    232    252       Potential.
FT   TOPO_DOM    253    334       Cytoplasmic (Potential).
FT   MOTIF       332    334       PDZ recognition motif (potential).
FT   CARBOHYD     60    60        N-linked (GlcNAc...) (Potential).
FT   DISULFID    135    135       By similarity.
FT   DISULFID     97    135       By similarity.
FT   DISULFID     85    149       By similarity.
SQ   SEQUENCE   334 AA;  36859 MW;  48AF556E9ED566CD5 CRC64;
```

RESULT 14

```
Qy    Query Match    33.9%;  Score 628;  DB 1;  Length 334;
      Best Local Similarity   39.7%;  Pred No. 1.4e-32;
      Matches  146;  Conservative  50;  Mismatches 100;  Indels  72;  Gaps   13;

Qy      8  PGGVR--VGALILLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVYLYPQIGDRLLDLLCPRA  65
               ||||:  |.|:|.|:|| |||||||||||||||||||||||||||:|||||||.||||
Db      4  PRGGRWLLGVLIALCRLAAPLAKSLEPVSWASGNPKFMSGKGLVIYPEIGDKLDIICPKA  63

Qy     66  RPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLW  125
               .| ||::. :||:|||||||||||||||||||||||||||:||||||||||||:|||||
Db     64  EPSKP----YDYVKLYLVKDQADACSTVMDPNVLVTCNRPEQEIRFTIKFQEFSPNTM  118

Qy    126  GHEFRSHHIDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMP  185
               |||:|:|::|||:||::||.|||||:.|||||||.|||||||||:|.||.:|.|||:|.|
Db    119  GLEFRQQDYFITSTSNGTLDGLENREGGVCQTRSMKIVWKVGQDP-NAVIPEQLTTSRP  177

Qy    186  MER--------DRGAAHSL----EPGKENLPGDPTSNA--TSRGAEGPLPPPSMPAVAGA  231
               |:|        ||.||:|     ||||:|||||||:||  |:||||||.||||||.||||
Db    178  SKEADNTVKIVTQSPRHKVPTVEEPGK---PGSVNQNGQETQGPSDGFL--SSKVAVFAA  232

Qy    232  AGG--------LALLLLGVAGAGGANCWRRRRAKPSESRH------PGPGSFGRG  272
               |||        ||:||| ||.|:||.||.||||||||||      |||||.|||
Db    233  IGAGCVIFILIIFLVVLLIKI---------RKRHRKHTQQRAAALSLSTLASPKCSGNA  283

Qy    273  GSLGLGGGGGMGPREAEPGELGIALRGGGAADPF  305
               ||.| |||||||||||||| |.|||||| ||.|
Db    284  GS-----------EPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQS  326

Qy    333  PPNIYYKV  340
               ||:|||||
Db    327  PANIYYKV  334
```

EFNB2_BRARE

```
ID   EFNB2_BRARE     STANDARD;      PRT;    332 AA.
AC   O73874;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ephrin-B2a precursor.
GN   Name=efnb2a; Synonyms=efnb2;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98438455; PubMed=9765210;
RA   Durbin L., Brennan C., Shiomi K., Cooke J., Barrios A.,
RA   Shanmugalingam S., Guthrie B., Lindberg R., Holder N.;
RT   "Eph signaling is required for segmentation and differentiation of the
RT   somites.";
RL   Genes Dev. 12:3096-3109(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21290827; PubMed=11397014; DOI=10.1006/dbio.2001.0281;
RA   Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
RA   Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;
RT   "Morphogenesis of prechordal plate and notochord requires intact
RT   eph/ephrin b signaling.";
```

```
RESULT 15
       Q90Z33 BRARE
ID     Q90Z33 BRARE PRELIMINARY;     PRT;   341 AA.
AC     Q90Z33;
```

Left entry

```
RL   Dev. Biol. 234:470-482(2001).
CC   -!- SUBUNIT: Binds to the receptor tyrosine kinase EPHB4.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: Inducible phosphorylation of tyrosine residues in the
CC       cytoplasmic domain (By similarity).
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC   -----------------------------------------------------------------
```

```
DR   EMBL; AJ004863; CAA06168.1; -; mRNA.
DR   EMBL; AF375225; AAK64275.1; -; mRNA.
DR   HSSP; P52800; 1IKO.
DR   Ensembl; ENSDARG00000020164; Danio rerio.
DR   ZFIN; ZDB-GENE-990415-67; efnb2a.
DR   GO; GO:0000039; P:synaptic target recognition; IEP.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Differentiation; Glycoprotein; Neurogenesis;
KW   Phosphorylation; Signal; Transmembrane.
FT   SIGNAL       1     24
FT   CHAIN       25    332       Ephrin-B2a.
FT   TOPO_DOM    25    225       Extracellular (Potential).
FT   TRANSMEM   226    246       Potential.
FT   TOPO_DOM   247    332       Cytoplasmic (Potential).
FT   MOTIF      330    332       PDZ recognition motif (Potential).
FT   CARBOHYD    20     20       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    33     33       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   136    136       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   211    211       N-linked (GlcNAc...) (Potential).
FT   DISULFID    59     98       By similarity.
FT   DISULFID    86    150       By similarity.
SQ   SEQUENCE   332 AA;  36724 MW;  189ED82372C71C8B CRC64;

Query Match             33.9%;
Best Local Similarity   42.2%;
Matches   145;  Conservative   54;  Mismatches  106;  Indels   39;  Gaps   12;
Score 626.5;  DB 1;  Length 332;
Pred. No. 1.8e-32;

Qy   14 GALLLLGVILGVILVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS  73
        |:|||:| |:|||||:|||||||||||||||||||||||||||:|||:| ||||:    ::|
Db   11 GVLVIACKVNLSRALILDSIYWNTNTNTKFVPGQOGCLVLVPQIGDKMDIVCPRVE---GGSM  67

Qy   74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH  133
        |:||:||| | |:|:||::  :| : || :|::  |: :|| ||||:|||||| ||| |:
Db   68 EGVEYYKYLYMVPLEQLKSCQVTKADTPLLNCVKPDQDDVKFTLKFQEFSSPNLWGLEFPRGK  127

Qy  134 DYYIIATSDGTTREGLESLIGGGVCLTRGMKVLLRVGQSPRGGAVPRK-PVSEMPEMERDRGA  192
        |||| :||:|  |||:.| ||||||::.|||:::.||:.:   : ||  | | ::    :||
Db  128 DYYIISTSNGTMEGLDNOGEGGVCKTKSMKIIMKVGQNPSDPISPKDYPTSYPKDHPDLGG  187

Qy  193 AHS-----LEP------GKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGIALLLLGV  242
        ..|     |::      | ::  ||:.: ||     | :|         .||::::||:|
Db  188 KDSKSNEVLKPDASPHGEDK---GDGNKSSSVIGSEVAL-----FACIASASVIVIIIIML  241

Qy  243 AGAGGAMCWRRRRAKPSESRHPGPGSFG-------RGGSLGLGGGGMGPREABPGELGIA  296
        . |:  ::  :::::. :   ::  |       | ||||   :||:.|   ::. |:  |
Db  242 VFL--LLKYRHRHKHS-PQHATTLSLSTLATPKRGGS-----GGNNNG---SEPSDIIIP  291

Qy  297 LRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPNIYYKV  340
        ||   :  | ||:||||||||||||||:||:.|||||:|||||
Db  292 LR---TADSVFCPHYEKVSGDYGHPVIVQEMPPQSPANIYYKV  332
```

Right entry

```
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ephrin B1.
GN   Name=efnb1;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21290827; PubMed=11397014; DOI=10.1006/dbio.2001.0281;
RA   Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
RA   Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;
RT   "Morphogenesis of prechordal plate and notochord requires intact
RT   eph/ephrin b signaling.";
RL   Dev. Biol. 234:470-482(2001).
DR   EMBL; AF375224; AAK64274.1; -; mRNA.
DR   HSSP; P52800; 1IKO.
DR   Ensembl; ENSDARG00000007723; Danio rerio.
DR   ZFIN; ZDB-GENE-010618-2; efnb1.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
SQ   SEQUENCE   341 AA;  37849 MW;  CB922F20B0D93E94 CRC64;

Query Match             33.3%;
Best Local Similarity   41.8%;
Matches   141;  Conservative   49;  Mismatches  109;  Indels   38;  Gaps   11;
Score 616;  DB 2;  Length 341;
Pred. No. 8.6e-32;

Qy   24 LVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYL  83
        |::  ||| ||||| ::|:|:| |:|::||:||::|:::|||    :| || :|||||||
Db   23 LPAAKSLSSVVWNSQONPKFVSGKGLIVIYPEIGDKLDIICPK---GDMGRP-YEFYKLYL  77

Qy   84 VGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDG  143
        | :|::  |.:  : |:|| || |:  : |||||||:|||::| ||:.:: ||| ||::|
Db   78 VKKEQAESCSTILLDPNVLLVTCNKPEKDIKFTIKFQEFSPNYMGLEFKRFTNYYITSTSNG  137

Qy  144 TREGLESLGGGVCLTRGMKVLLRVGQSPRG-----GAVPRKPVSEMPEMERDRGAAHSLEP  198
        | |||:.. ||||.|. ||:::.||:.    :   || ::   |::     :   .:| :
Db  138 TOEGLENREGGVCSTRSMKIIMKVGQDPNAPDDPLPDLPDRPYDNEIKDPTTSPSRKTER  197

Qy  199 GKEN------LPGDPTSNATSR--GAEGPLPPPSMPAVAGAAG-GLALLLLGVAGAGG  247
        | :.      ||||:.:     ||:| |  ||::   .: |  |: :: : .|:
Db  198 GRENEVDGNGSRMPGKDTRNQNNSPGSVEGIF--GSKPALFAAIGAGCVIFLLIILIV  255

Qy  248 AMCWRRRRAKPSESRHPGPGSFGRGGGSL----GLGGGGMGPREAEPGELGIALRGGGAA  303
        ::  :::: | .:   | |   | || |     |:   |   :.:  : :  .||   :
Db  256 LLILKLRKTR----KHSQP-----RGGTALSLSTLATPKGAAQAGSEPSDIIIPLR---TT  304

Qy  304 DPPFCPHYEKVSGDYGHPVYIVQDGPPQSPNIYYKV  340
        :  .|||||||||||||||:||:..||||||:||||
Db  305 ENNYCPHYEKVSGDYGHPVIVQEMPPQSPANIYYKV  341
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OM protein - protein search, using sw model

                          Copyright (c) 1993 - 2005  Compugen Ltd.
                          GenCore version 5.1.6

Run on:         December 21, 2005, 14:25:04 ; Search time 27.7987 Seconds
                                             (without alignments)
                                             1011.187 Million cell updates/sec

Title:          US-10-021-121-4
Perfect score:  1850
Sequence:       1 MGPPHSGPGGVRVGALLLLG.........PVYIVQDGPPQSPPNIYYKV 340

Scoring table:  BLOSUM62
                Gapop 10.0 , Gapext 0.5

Searched:       572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters:     572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      Issued_Patents_AA:*
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                2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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                4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                  SUMMARIES

Result          %      Query
No.    Score  Match  Length DB   ID                  Description
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 1     1850  100.0    340   2    US-08-635-130A-4     Sequence 4, Appli
 2     1850  100.0    340   2    US-09-949-016-6076   Sequence 6076, Ap
 3     1850  100.0    397   2    US-09-949-016-10967  Sequence 10967, A
 4     1846   99.8    340   2    US-09-214-631-3      Sequence 3, Appli
 5     1844   99.7    340   2    US-09-051-994-2      Sequence 2, Appli
 6     1841   99.5    455   2    US-08-635-130A-2     Sequence 2, Appli
 7     637.5   34.5   336   1    US-08-436-044-2      Sequence 2, Appli
 8     637.5   34.5   336   1    US-08-436-054-2      Sequence 2, Appli
 9     637.5   34.5   336   4    PCT-US95-08812-2     Sequence 2, Appli
10     632     34.2   346   2    US-08-213-403-2      Sequence 2, Appli
11     632     34.2   346   1    US-08-458-077-2      Sequence 2, Appli
12     632     34.2   346   1    US-08-467-741-2      Sequence 2, Appli
13     632     34.2   346   1    US-08-747-240-2      Sequence 2, Appli
14     632     34.2   346   1    US-08-299-567-6      Sequence 6, Appli
15     632     34.2   346   2    US-09-039-642B-2     Sequence 2, Appli
16     632     34.2   346   2    US-09-035-130A-9     Sequence 9, Appli
17     632     34.2   522   1    US-09-949-016-11189  Sequence 11189, A
18     629.5   34.0   333   1    US-08-436-054-4      Sequence 4, Appli
19     629.5   34.0   333   2    US-08-271-948-2      Sequence 2, Appli
20     629.5   34.0   333   2    US-08-436-054-4      Sequence 4, Appli
21     629.5   34.0   333   2    US-09-733-333-2      Sequence 2, Appli
22     629.5   34.0   333   2    US-09-754-105-2      Sequence 2, Appli
23     629.5   34.0   333   2    US-09-978-339-2      Sequence 2, Appli
24     629.5   34.0   333   2    US-08-635-130A-10    Sequence 10, Appl
25     629.5   34.0   333   4    US-09-949-016-6453   Sequence 6453, Ap
26     629.5   34.0   333   4    PCT-US95-08534-2     Sequence 2, Appli
27     629.5   34.0   333   4    PCT-US95-08812-4     Sequence 4, Appli
28     622.5   33.6   333   2    US-09-214-631-4      Sequence 4, Appli
29     608.5   32.9   345   2    US-09-214-631-5      Sequence 5, Appli
30     572.5   30.9   303   2    US-09-949-016-9295   Sequence 9295, Ap
31     498     26.9   89    2    US-09-214-631-13     Sequence 13, Appl
32     200.5   10.9   82    2    US-09-214-631-11     Sequence 11, Appl
33     200.5   10.8   82    2    US-09-214-631-12     Sequence 12, Appl
34     179      9.7   234   1    US-08-299-567-5      Sequence 5, Appli
35     179      9.7   238   1    US-09-949-002-378    Sequence 378, App
36     179      9.7   238   1    US-08-240-124-2      Sequence 2, Appli
37     179      9.7   238   2    US-09-949-002-413    Sequence 413, Appl
38     179      9.7   238   2    US-08-453-943-2      Sequence 2, Appli
39     179      9.7   238   2    US-09-057-121-2      Sequence 2, Appli
40     179      9.7   238   1    US-09-358-734-2      Sequence 2, Appli
41     176.5    9.5   135   1    US-08-299-567-5      Sequence 7, Appli
42     176.5    9.5   135   2    US-08-920-440B-2     Sequence 5, Appli
43     176      9.5   184   2    US-08-299-567-5      Sequence 2, Appli
44     176      9.5   184   1    US-09-173-492-2      Sequence 2, Appli
45     176      9.5   184   2    US-09-173-133-2      Sequence 2, Appli
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ALIGNMENTS

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RESULT 1
US-08-635-130A-4
Sequence 4, Application US/08635130A
; Patent No. 6696557
; GENERAL INFORMATION:
;  APPLICANT: Caras, Ingrid W
;  TITLE OF INVENTION: A2-1 Neurotrophic Factor
;  NUMBER OF SEQUENCES: 10
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 1 DNA Way
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatin (Genentech)
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/635,130A
;   FILING DATE: 19-Mar-1996
;   CLASSIFICATION: 435
;  ATTORNEY/AGENT INFORMATION:
;   NAME: Torchia, PhD., Timothy E.
;   REGISTRATION NUMBER: 36,700
;   REFERENCE/DOCKET NUMBER: P1001
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650/225-8674
;   TELEFAX: 650/952-9881
;  INFORMATION FOR SEQ ID NO:  4:
;   SEQUENCE CHARACTERISTICS:
;    LENGTH: 340 amino acids
;    TYPE: Amino Acid
;    TOPOLOGY: Linear
US-08-635-130A-4

  Query Match             100.0%;  Score 1850; DB 2;  Length 340;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-148;
  Matches  340;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
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RESULT 2
US-09-949-016-6076
Sequence 6076, Application US/0994916
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6076
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6076

Query Match   100.0%; Score 1850; DB 2; Length 340;
Best Local Similarity   100.0%; Pred. No. 1.1e-148;
Matches 340; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy    1 MGPPHSGPGGVRVGALLLLGVLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
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Db    1 MGPPHSGPGGVRVGALLLLGVLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy   61 LCPRARPPGPHSSPNYEYKLYLYGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LCPRARPPGPHSSPNYEYKLYLYGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy  121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy  181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy  241 GVAGAGGAMCWRRRARAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GVAGAGGAMCWRRRARAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG 300

Qy  301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
        ||||||||||||||||||||||||||||||||||||||||
Db  301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
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RESULT 3
US-09-949-016-10967
Sequence 10967, Application US/0994916
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10967
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10967

Query Match   100.0%; Score 1850; DB 2; Length 397;
Best Local Similarity   100.0%; Pred. No. 1.3e-148;
Matches 340; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy    1 MGPPHSGPGGVRVGALLLLGVLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
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Qy   61 LCPRARPPGPHSSPNYEYKLYLYGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy  121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  178 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 237

Qy  181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  238 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 297

Qy  241 GVAGAGGAMCWRRRARAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  298 GVAGAGGAMCWRRRARAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG 357

Qy  301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
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Db  358 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 397
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RESULT 4
US-09-214-631-3
Sequence 3, Application US/09214631
; Patent No. 6413730
; GENERAL INFORMATION:
; APPLICANT: Holland, Sacha
; APPLICANT: Mbamalu, Geraldine
; APPLICANT: Pawson, Tony
; TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
; TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
; TITLE OF INVENTION: TYROSINE KINASES
; FILE REFERENCE: 11757.23USWO
; CURRENT APPLICATION NUMBER: US/09/214,631
; CURRENT FILING DATE: 1999-03-12
; EARLIER APPLICATION NUMBER: US/09/214,631
; EARLIER FILING DATE: 1997-07-04
; EARLIER APPLICATION NUMBER: PCT/CA97/00473
; EARLIER FILING DATE: 1997-07-04
; EARLIER APPLICATION NUMBER: 60/021,272
; EARLIER FILING DATE: 1996-07-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3

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;   LENGTH: 340
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-214-631-3

Query Match      99.8%;  Score 1846;  DB 2;  Length 340;
Best Local Similarity   99.7%;  Pred. No. 2.4e-148;
Matches 339;  Conservative 1;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   1 MGPPHSGPGGVRVGALLLGVLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
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Db   1 MGPPHSGPGGVRVGALLLGVLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy  61 LCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
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Db  61 LCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy 121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy 181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL 240
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Db 181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL 240

Qy 241 GVAGAGGAMCWRRRRAKPSESSRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
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Db 241 GVAGAGGAMCWRRRRAKPSESSRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy 301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYYKV 340
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Db 301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYYKV 340


RESULT 5
US-09-051-994-2
;  Sequence 2, Application US/09051994A
;  Patent No. 6602683
;  GENERAL INFORMATION:
;     APPLICANT: REGENERON PHARMACEUTICALS, INC.
;     TITLE OF INVENTION: BIOLOGICALLY ACTIVE EPH FAMILY LIGANDS
;     FILE REFERENCE: REG-341-PCT-US
;     CURRENT APPLICATION NUMBER: US/09/051,994A
;     CURRENT FILING DATE: 1998-04-24
;     EARLIER APPLICATION NUMBER: PCT/US96/17201
;     EARLIER FILING DATE: 1996-10-25
;     EARLIER APPLICATION NUMBER: 60/007,015
;     EARLIER FILING DATE: 1995-10-25
;     NUMBER OF SEQ ID NOS: 3
;     SOFTWARE: PatentIn Ver. 2.0
;  SEQ ID NO 2
;     LENGTH: 340
;     TYPE: PRT
;     ORGANISM: Homo sapiens
;     FEATURE:
;     NAME/KEY: site
;     LOCATION: (166)
;     OTHER INFORMATION: Xaa=Arg or Gln
US-09-051-994-2

Query Match      99.7%;  Score 1844;  DB 2;  Length 340;
Best Local Similarity   99.7%;  Pred. No. 3.5e-148;
Matches 339;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

Qy   1 MGPPHSGPGGVRVGALLLGVLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGPPHSGPGGVRVGALLLGVLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy  61 LCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 LCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy 121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy 181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL 240
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL 240

Qy 241 GVAGAGGAMCWRRRRAKPSESSRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241 GVAGAGGAMCWRRRRAKPSESSRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy 301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYYKV 340
       ||||||||||||||||||||||||||||||||||||||||
Db 301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYYKV 340


RESULT 6
US-08-635-130A-2
;  Sequence 2, Application US/08635130A
;  Patent No. 6696557
;  GENERAL INFORMATION:
;     APPLICANT: Caras, Ingrid W
;     TITLE OF INVENTION: A2-1 Neurotrophic Factor
;     NUMBER OF SEQUENCES: 10
;     CORRESPONDENCE ADDRESS:
;        ADDRESSEE: Genentech, Inc.
;        STREET: 1 DNA Way
;        CITY: South San Francisco
;        STATE: California
;        COUNTRY: USA
;        ZIP: 94080
;     COMPUTER READABLE FORM:
;        MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;        COMPUTER: IBM PC compatible
;        OPERATING SYSTEM: PC-DOS/MS-DOS
;        SOFTWARE: WinPatin (Genentech)
;     CURRENT APPLICATION DATA:
;        APPLICATION NUMBER: US/08/635,130A
;        FILING DATE: 19-Mar-1996
;        CLASSIFICATION: 435
;     ATTORNEY/AGENT INFORMATION:
;        NAME: Torchia, PhD., Timothy E.
;        REGISTRATION NUMBER: 36,700
;        REFERENCE/DOCKET NUMBER: P1001
;     TELECOMMUNICATION INFORMATION:
;        TELEPHONE: 650/225-8674
;        TELEFAX: 650/952-9881
;  INFORMATION FOR SEQ ID NO: 2:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH: 455 amino acids
;        TYPE: Amino Acid
;        TOPOLOGY: Linear
US-08-635-130A-2

Query Match      99.5%;  Score 1841;  DB 2;  Length 455;
Best Local Similarity   100.0%;  Pred. No. 9e-148;
Matches 338;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   1 MGPPHSGPGGVRVGALLLGVLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGPPHSGPGGVRVGALLLGVLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy  61 LCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 LCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy 121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy 181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL 240
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL 240
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RESULT 7
US-08-436-044-2
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; Sequence 2, Application US/08436044
; Patent No. 562489
; GENERAL INFORMATION:
;   APPLICANT:  Bennett, Brian D.
;   APPLICANT:  Matthews, William
;   TITLE OF INVENTION:  HTK LIGAND
;   NUMBER OF SEQUENCES:  7
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Genentech, Inc.
;     STREET:  460 Point San Bruno Blvd
;     CITY:  South San Francisco
;     STATE:  California
;     COUNTRY:  USA
;     ZIP:  94080
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  patin (Genentech)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/436,044
;     FILING DATE:  05-MAY-1995
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/277722
;     FILING DATE:  20-JUL-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Lee, Wendy M.
;     REGISTRATION NUMBER:  00,000
;     REFERENCE/DOCKET NUMBER:  902D3
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  415/225-1994
;     TELEFAX:  415/952-9881
;     TELEX:  910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  336 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
US-08-436-044-2

Query Match             34.5%;  Score 637.5;  DB 1;  Length 336;
Best Local Similarity   42.1%;  Pred. No. 4.9e-46;
Matches  139;  Conservative  49;  Mismatches 129;  Indels  13;  Gaps   5;

Qy     14 GALLLLGVLGLVSGLSLSEPYVWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
          |||:|||   :|:|:| :|||||.||||||.|:|:||||||||||.|||:||||   ||||
Db     17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73

Qy     74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
          ::|:|.||:|:|.||||.|   ||||||:.|:||||:|:||||||||:||||||:||::|.
Db     74 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133

Qy    134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
          ||||::|| |: |||:.|:.|||.||.|.|:|:.|||  .|:|.:|:|||:|||:||: |.
Db    134 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

Qy    191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
          |:::| .:|.:||||:.|:|.|::|.||:|| ::||.||:|:|:||.||||:|||||||:
Db    194 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL 253

Qy    241 GVAGAGGAMCWRRRAKPSESESRIPGPGSFGRGGSLGLGGGGMGPREABPGELGIALRGG 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GVAGAGGAMCWRRRAKPSESESRIPGPGSFGRGGSLGLGGGGMGPREABPGELGIALRGG 300

Qy    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPPQSPPNIIY 338
          ||||||||||||||||||||||||||||||||||||||
Db    301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPPQSPPNIIY 338
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RESULT 8
US-08-436-054-2
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; Sequence 2, Application US/08436054
; Patent No. 5864020
; GENERAL INFORMATION:
;   APPLICANT:  Bennett, Brian D.
;   APPLICANT:  Matthews, William
;   TITLE OF INVENTION:  HTK LIGAND
;   NUMBER OF SEQUENCES:  7
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Genentech, Inc.
;     STREET:  460 Point San Bruno Blvd
;     CITY:  South San Francisco
;     STATE:  California
;     COUNTRY:  USA
;     ZIP:  94080
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  patin (Genentech)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/436,054
;     FILING DATE:  05-MAY-1995
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/277722
;     FILING DATE:  20-JUL-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Lee, Wendy M.
;     REGISTRATION NUMBER:  00,000
;     REFERENCE/DOCKET NUMBER:  902D1
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  415/225-1994
;     TELEFAX:  415/952-9881
;     TELEX:  910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  336 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
US-08-436-054-2

Query Match             34.5%;  Score 637.5;  DB 1;  Length 336;
Best Local Similarity   42.1%;  Pred. No. 4.9e-46;
Matches  139;  Conservative  49;  Mismatches 129;  Indels  13;  Gaps   5;

Qy     14 GALLLLGVLGLVSGLSLSEPYVWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
          |||:|||   :|:|:| :|||||.||||||.|:|:||||||||||.|||:||||   ||||
Db     17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73

Qy     74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
          ::|:|.||:|:|.||||.|   ||||||:.|:||||:|:||||||||:||||||:||::|.
Db     74 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133

Qy    134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
          ||||::|| |: |||:.|:.|||.||.|.|:|:.|||  .|:|.:|:|||:|||:||: |.
Db    134 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

Qy    191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
          |:::| .:|.:||||:.|:|.|::|.||:|| ::||.||:|:|:||.||||:|||||||:
Db    194 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL 253

Qy    251 WRRRAKPSESESRIPGPGSFGRGGSLGLGGGGMGPREABPGELGIALRGGGAADPPFCPH 310
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    251 WRRRAKPSESESRIPGPGSFGRGGSLGLGGGGMGPREABPGELGIALRGGGAADPPFCPH 310

Qy    311 YEKVSGDYGHPVVIVQDGPPPQSPPNIIYKV 340
          ||||||||||||||||||:  |||||:||||
Db    307 YEKVSGDYGHPVVIVQDEMPPQSPANIIYKV 336
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Db    254  KYRRHRKHSPQHTTLSLSTLLATPKRGGNN-----NGSEPSDVIIPLR---TADSVFCPH   306
           |||   |  :  :||||||  |::  |   |      |||||||| |||     |||  ||||
Qy    311  YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV   340
           ||||||||||||||||  |  ||||||||||
Db    307  YEKVSGDYGHPVYIVQEMPPQSPANIYYKV   336
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RESULT 9
PCT-US95-08812-2
Sequence 2, Application PCT/TUS9508812
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: HTK LIGAND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08812
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 902PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US95-08812-2

Query Match   34.5%; Score 637.5; DB 4; Length 336;
Best Local Similarity 42.1%; Pred. No. 4.9e-46;
Matches 139; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

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Qy    14  GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGHSS    73
          |:|| || :: :|||||:|||||:|:|  |  |||||||||||:||:|||| |      :
Db    17  GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGGGLVLYPQIGDKLDIICPKV---DSKTV   73

Qy    74  PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH   133
Db    74  GQYEYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK    133

Qy   134  DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPER-DR   190
Db   134  DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN  193

Qy   191  GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPSMPAVAGAGAGLALLLLGVAGAGGAMC   250
Db   194  GRSSTTSPFVKNPGSSTDGNSAGHSGNNLLGSEVALPAGIASGCIIPIVIITLVVLLL    253

Qy   251  WRRRRAKPSESRHPGGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH  310
Db   254  KYRRHRKHSPQHTTLSLSTLLATPKRGGNN-----NGSEPSDVIIPLR---TADSVFCPH  306
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Qy    311  YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV   340
           ||||||||||||||||  |  ||||||||||
Db    307  YEKVSGDYGHPVYIVQEMPPQSPANIYYKV   336
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RESULT 10
US-08-213-403-2
; Patent No. 5512457
Sequence 2, Application US/08213403
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; APPLICANT: Baum, Peter R.
; APPLICANT: Carpenter, Melissa
; TITLE OF INVENTION: No. 5512457e1 Cytokine Designated elk Ligand
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/213,403
; FILING DATE: 15-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,693
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-213-403-2

Query Match   34.2%; Score 632; DB 1; Length 346;
Best Local Similarity 39.5%; Pred. No. 1.5e-45;
Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

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Qy     8  PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL    61
Db     4  PGQRWLGKWLVAMVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII   63

Qy    62  CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS  121
Db    64  CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS  118

Qy   122  PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV  181
Db   119  PNIWGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT  178

Qy   182  SEMPERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPSMPAVAGAGAGLA----   236
Db   179  SRPSKEADNTVRMATQAPGSRGSLGDSDGKHETVNQEEKSGP-------GASGGSSGDPD  231

Qy   237  -----LLILGVAGAGGA-----MCWRRRRAKPSESRHPGGPGSFGRGGSLGL        277
Db   232  GFFNSKVALFAAVGAGCVIFLLIIFLTVLLLKLRKRHRKHTQQ--------RAAALSL    282
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RESULT 11
US-08-458-077-2
; Sequence 2, Application US/08458077
; Patent No. 5627267
; GENERAL INFORMATION:
; APPLICANT:  Lyman, Stewart D.
; APPLICANT:  Beckmann, M. Patricia
; APPLICANT:  Baum, Peter R
; APPLICANT:  Carpenter, Melissa
; TITLE OF INVENTION: No. 5627267e1 Cytokine Designated elk Ligand
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Immunex Corporation
; STREET:  51 University Street
; CITY:  Seattle
; STATE:  Washington
; COUNTRY:  USA
; ZIP:  98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  Apple Macintosh
; OPERATING SYSTEM:  Apple System 7.1
; SOFTWARE:  Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/08/458,077
; FILING DATE:  01-JUN-1995
; CLASSIFICATION:  514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:  US 08/213,403
; FILING DATE:  15-MAR-1994
; APPLICATION NUMBER:  US 07/977,693
; FILING DATE:  13-NOV-1992
; CLASSIFICATION:  514
; ATTORNEY/AGENT INFORMATION:
; NAME:  Seese, Kathryn A.
; REGISTRATION NUMBER:  32,172
; REFERENCE/DOCKET NUMBER:  2807-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  (206) 587-0430
; TELEFAX:  (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH:  346 amino acids
; TYPE:  amino acid
; TOPOLOGY:  linear
; MOLECULE TYPE:  protein
US-08-458-077-2

Query Match            34.2%;  Score 632;  DB 1;  Length 346;
Best Local Similarity  39.5%;  Pred. No. 1.5e-45;
Matches  145;  Conservative  48;  Mismatches 116;  Indels 58;  Gaps 9;

Qy  278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                 ||||  |::|||::||   |:::||||||||||||||||||||||||
Db  283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQBMPPQSP 339

Qy  334 PNIYYKV 340
            |||||||
Db  340 ANIYYKV 346

Qy    8 PGGVRVGALLLLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
            || :|| ||| |:| |||         | :|| ||:|||  |||:|||||||  | |:
Db    4 PGQRWLGKWLIVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy   62 CPRARPPGPHSSPNYEFYKLYLIVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
            |||| | ||:|||::||:|||:|| |   ||::  |  |||| ||| |||:||||||:|
Db   64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy  122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKYLLRVGCQSPRGGAVERKPV 181
            ||| ||| :||:||||| | |||  |:|  |:  |:|||||||:::::  ::|  |  |
Db  119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178
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RESULT 12
US-08-460-741-2
; Sequence 2, Application US/08460741
; Patent No. 5670625
; GENERAL INFORMATION:
; APPLICANT:  Lyman, Stewart D.
; APPLICANT:  Beckmann, M. Patricia
; APPLICANT:  Baum, Peter R
; APPLICANT:  Carpenter, Melissa
; TITLE OF INVENTION: No. 5670625e1 Cytokine Designated elk Ligand
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Immunex Corporation
; STREET:  51 University Street
; CITY:  Seattle
; STATE:  Washington
; COUNTRY:  USA
; ZIP:  98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  Apple Macintosh
; OPERATING SYSTEM:  Apple System 7.1
; SOFTWARE:  Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER:  US/08/460,741
; FILING DATE:  02-JUN-1995
; CLASSIFICATION:  530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:  US 08/213,403
; FILING DATE:  15-MAR-1994
; APPLICATION NUMBER:  US 07/977,693
; FILING DATE:  13-NOV-1992
; CLASSIFICATION:  530
; ATTORNEY/AGENT INFORMATION:
; NAME:  Seese, Kathryn A.
; REGISTRATION NUMBER:  32,172
; REFERENCE/DOCKET NUMBER:  2807-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:  (206) 587-0430
; TELEFAX:  (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH:  346 amino acids
; TYPE:  amino acid
; TOPOLOGY:  linear
; MOLECULE TYPE:  protein
US-08-460-741-2

Query Match            34.2%;  Score 632;  DB 1;  Length 346;
Best Local Similarity  39.5%;  Pred. No. 1.5e-45;
Matches  145;  Conservative  48;  Mismatches 116;  Indels 58;  Gaps 9;

Qy  182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA--- 236
              :  | |:   |       |:|| ||  | ||  |:| |:   |       |  |
Db  179 SRPSKEADNTVKMATQAPSRGSLGDSDPGKHETVNQEEKSGP-------GASGSSGDPD 231

Qy  237 ------LILGVAGGAGGA------MCWRRRAKPSESRHPGPSGFGRGGSLGL 277
                      |  |||||        | :   :|  |  | |  |  |  |
Db  232 GFFNSKVALFAAVGAGCVTFLLIIIFLTVLLLKLRKRHRKHTQQ------RAAALSL 282

Qy  278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                 ||||  |::|||::||   |:::||||||||||||||||||||||||
Db  283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQBMPPQSP 339

Qy  334 PNIYYKV 340
            |||||||
Db  340 ANIYYKV 346

Qy    8 PGGVRVGALLLLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
            || :|| ||| |:| |||         | :|| ||:|||  |||:|||||||  | |:
Db    4 PGQRWLGKWLIVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
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RESULT 13
US-08-747-240-2
; Sequence 2, Application US/08747240
; Patent No. 5728813
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; APPLICANT: Baum, Peter R
; APPLICANT: Carpenter, Melissa
; TITLE OF INVENTION: No. 5728813e1 Cytokine Designated elk Ligand
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Immunex Corporation
;   STREET: 51 University Street
;   CITY: Seattle
;   STATE: Washington
;   COUNTRY: USA
;   ZIP: 98101
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: Apple Macintosh
;   OPERATING SYSTEM: Apple System 7.1
;   SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/747,240
;   FILING DATE: 12-NOV-1996
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/213,403
;   FILING DATE: 15-MAR-1994
;   APPLICATION NUMBER: US 07/977,693
;   FILING DATE: 13-NOV-1992
;   CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;   NAME: Seese, Kathryn A.
;   REGISTRATION NUMBER: 32,172
;   REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (206) 587-0430
;   TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 346 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-747-240-2

Qy   62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
Db   64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy 122 PNLWGHEFRSHHDYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
Db 119 PNYMGLEFKKHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVVGQDPNAVTPEQLTT 178

Qy 182 SEMPMERDRGAAHSLE-PGKENLPGDFPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
Db 179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP------GASGGSSGDPD 231

Qy 237 ------LILLGVAGGGA------------MCWRRRAKPSESRHPGPGSFGRGGSLGL 277
Db 232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKHRKHTQQ------RAAALSL 282

Qy 278 ----GGGGGMGPREAEPGELGIALRGGGAADPPPCPHYEKVSGDYGHPVYIVQDGPPQSP 333
Db 283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVIVQEMPPQSP 339

Qy 334 PNIYYKV 340
Db 340 ANIYYKV 346

RESULT 14
US-08-299-567-6
; Sequence 6, Application US/08299567
; Patent No. 5747033
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
; TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Regeneron Pharmaceuticals, Inc.
;   STREET: 777 Old Saw Mill River Road
;   CITY: Tarrytown
;   STATE: New York
;   COUNTRY: U.S.A.
;   ZIP: 10591-6707
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/299,567
;   FILING DATE: 01-SEP-1994
;   CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;   NAME: Kempler, Gail M.
;   REGISTRATION NUMBER: 32,143
;   REFERENCE/DOCKET NUMBER: REG 290
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 914-345-7400
;   TELEFAX: 914-345-7721
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 346 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: unknown
; MOLECULE TYPE: protein

Query Match   34.2%; Score 632; DB 1; Length 346;
Best Local Similarity   39.5%; Pred. No. 1.5e-45;
Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

Qy   8 PGGVRVGALLILGVLGLVSGL-------SLEPVYWNSANKRFQAEGGYVLLYPQIGDRLDLL 61
Db   4 PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLIVIYPKIGDKLDII 63

Qy   62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
Db   4 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy 122 PNLWGHEFRSHHDYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
Db 119 PNYMGLEFKKHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVVGQDPNAVTPEQLTT 178

Qy 182 SEMPMERDRGAAHSLE-PGKENLPGDFPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
Db 179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP------GASGGSSGDPD 231

Qy 237 ------LILLGVAGGGA------------MCWRRRAKPSESRHPGPGSFGRGGSLGL 277
Db 232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKHRKHTQQ------RAAALSL 282

Qy 278 ----GGGGGMGPREAEPGELGIALRGGGAADPPPCPHYEKVSGDYGHPVYIVQDGPPQSP 333
Db 283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVIVQEMPPQSP 339

Qy 334 PNIYYKV 340
Db 340 ANIYYKV 346

US-08-299-567-6

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Query Match       34.2%;   Score 632;  DB 1;  Length 346;
Best Local Similarity  39.5%;  Pred. No. 1.5e-45;
Matches  145;  Conservative  48;  Mismatches  116;  Indels  58;  Gaps  9;

Qy    8 PGGVRVGALLLGVLIGLVSGL------SLEPVYWNSANKRFQAEGGYYLYPQIGDRLDLL  61
          ||| ::||| |||  |  || ||           | ||  |  |:  ||||||| ||| ||
Db    4 PGQRWLGKWLVAMVWWALCRLATPLAKNLBPVSWSSLNPKFLSGKGLVIYPKIGDKLDII  63

Qy   62 CPRARPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS  121
          ||| | |::  ||| :||||| |   :  | |   |||||||:||||: |||||||||| :|
Db   64 CPRAEAGRP-----YEYYKLYLVRPBQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS  118

Qy  122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV  181
          || :| ||: ||||||::::::| :||| :|:::| |:: :|:::::| ||  :  ||:
Db  119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRRTMKIIMKVGQDPNAVTPEQLTT   178

Qy  182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA----  236
          :  :: |   ::|    || : |||:|  | :| | :  :    | | :    ::| :
Db  179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP------GASGGSSGDPD   231

Qy  237 -----------LILLGVAGAGGA------------MCWRRRAKPSSSRHPGPGSFGRGGSLGL  277
                    ||| ||| ||            |||  :  |:  :  :|| : | |: |
Db  232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRIHRKHTQQ------RAAALSL    282

Qy  278 ---GGGGGGMGPRBAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP  333
             ||  | | |  |  |  | :  | |:|  |:||||||||||||||||||| :  ||||
Db  283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP  339

Qy  334 PNIYYKV 340
          :|||||
Db  340 ANIYYKV 346
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Db   64 CPRAEAGRP-----YEYYKLYLVRPBQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS  118
Qy  122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV  181
Db  119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRRTMKIIMKVGQDPNAVTPEQLTT   178
Qy  182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA----  236
Db  179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP------GASGGSSGDPD   231
Qy  237 -----------LILLGVAGAGGA------------MCWRRRAKPSSSRHPGPGSFGRGGSLGL  277
Db  232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRIHRKHTQQ------RAAALSL    282
Qy  278 ---GGGGGGMGPRBAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP  333
Db  283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP  339
Qy  334 PNIYYKV 340
Db  340 ANIYYKV 346
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Search completed: December 21, 2005, 14:37:39
Job time : 28.7987 secs

RESULT 15
US-09-039-642B-2

Sequence 2, Application US/09039642B
Patent No. 6540992
GENERAL INFORMATION:
APPLICANT: Lyman, Stewart D.
APPLICANT: Beckmann, M. Patricia
APPLICANT: Baum, Peter R.
APPLICANT: Carpenter, Melissa K.
TITLE OF INVENTION: NOVEL CYTOKINE DESIGNATED ELK LIGAND
FILE REFERENCE: GENENT.67CPDV3
CURRENT APPLICATION NUMBER: US/09/039,642B
CURRENT FILING DATE: 1998-03-16
PRIOR APPLICATION NUMBER: 08/213,403
PRIOR FILING DATE: 1994-03-15
PRIOR APPLICATION NUMBER: 07/977,693
PRIOR FILING DATE: 1992-11-13
PRIOR APPLICATION NUMBER: 08/747,240
PRIOR FILING DATE: 1996-10-12
PRIOR APPLICATION NUMBER: 08/460,741
PRIOR FILING DATE: 1995-06-02
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens
US-09-039-642B-2

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Query Match       34.2%;   Score 632;  DB 2;  Length 346;
Best Local Similarity  39.5%;  Pred. No. 1.5e-45;
Matches  145;  Conservative  48;  Mismatches  116;  Indels  58;  Gaps  9;

Qy    8 PGGVRVGALLLGVLIGLVSGL------SLEPVYWNSANKRFQAEGGYYLYPQIGDRLDLL  61
          ||| ::||| |||  |  || ||           | ||  |  |:  ||||||| ||| ||
Db    4 PGQRWLGKWLVAMVWWALCRLATPLAKNLBPVSWSSLNPKFLSGKGLVIYPKIGDKLDII  63

Qy   62 CPRARPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS  121
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OM protein - protein search, using sw model

Copyright (c) 1993 - 2005 Compugen Ltd.
GenCore version 5.1.6

Run on: December 21, 2005, 14:30:39 ; Search time 95.7987 Seconds
(without alignments)
1482.921 Million cell updates/sec

Title: US-10-021-121-4
Perfect score: 1850
Sequence: 1 MGPPHSGPGGVRVGALLLLG.........PVYIVQDGPPQSPNIYYKV 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1850	100.0	340	4	US-10-021-121-4	Sequence 4, Appli
2	1850	100.0	340	4	US-10-723-860-4256	Sequence 4256, Ap
3	1850	100.0	340	5	US-10-699-907-16	Sequence 16, Appl
4	1846	99.8	340	4	US-10-138-787-3	Sequence 3, Appli
5	1844	99.7	340	4	US-10-417-924A-2	Sequence 2, Appli
6	1841	99.5	455	4	US-10-021-121-2	Sequence 2, Appli
7	1780	96.2	340	4	US-10-698-907-8	Sequence 8, Appli
8	1559	84.3	285	4	US-10-408-765A-2695	Sequence 2695, Ap
9	637.5	34.5	336	5	US-10-699-907-7	Sequence 7, Appli
10	632	34.2	346	4	US-10-021-121-9	Sequence 9, Appli
11	632	34.2	346	4	US-10-356-289-2	Sequence 2, Appli
12	632	34.2	346	5	US-10-711-124-60	Sequence 60, Appl
13	632	34.2	346	5	US-10-789-378-30	Sequence 30, Appl
14	632	34.2	346	4	US-10-698-907-14	Sequence 14, Appl
15	629.5	34.0	333	3	US-09-754-105-2	Sequence 2, Appli
16	629.5	34.0	333	4	US-09-978-339-2	Sequence 2, Appli
17	629.5	34.0	333	4	US-10-408-765A-2695	Sequence 2695, Ap
18	629.5	34.0	333	5	US-10-331-496A-63	Sequence 63, Appl
19	629.5	34.0	333	4	US-10-021-121-10	Sequence 10, Appl
20	629.5	34.0	333	5	US-10-698-907-15	Sequence 15, Appl
21	629.5	34.0	333	5	US-10-800-350-396	Sequence 396, App
22	629.5	34.0	333	4	US-10-800-077-396	Sequence 396, Appl
23	622.5	33.6	333	4	US-10-138-787-4	Sequence 4, Appli
24	613.5	33.2	345	5	US-10-699-907-6	Sequence 6, Appli
25	608.5	32.9	345	4	US-10-138-787-5	Sequence 5, Appli
26	498	26.9	89	3	US-09-862-179A-17	Sequence 17, Appl
27	498	26.9	89	4	US-10-138-787-13	Sequence 13, Appl
28	447	24.2	229	5	US-10-698-907-20	Sequence 20, Appl
29	446.5	24.1	459	5	US-10-800-350-390	Sequence 390, App
30	446.5	24.1	226	5	US-10-800-077-390	Sequence 390, App
31	443	23.9	233	5	US-10-698-907-21	Sequence 21, Appl
32	442	23.9	233	5	US-10-800-350-388	Sequence 388, App
33	442	23.9	233	5	US-10-800-077-388	Sequence 388, App
34	284.5	15.4	92	5	US-09-864-761-48262	Sequence 48262, A
35	205.5	11.1	136	3	US-09-864-761-48257	Sequence 48257, A
36	202.5	10.9	106	3	US-09-925-297-639	Sequence 639, App
37	201	10.9	82	4	US-10-862-179A-15	Sequence 15, Appl
38	201	10.9	82	4	US-10-138-787-11	Sequence 11, Appl
39	200.5	10.8	82	3	US-09-862-179A-16	Sequence 16, Appl
40	200.5	10.8	82	4	US-10-138-787-12	Sequence 12, Appl
41	182	9.8	652	6	US-11-097-143-2655	Sequence 2655, Ap
42	182	9.8	652	6	US-11-097-143-23436	Sequence 23436, A
43	179	9.7	238	5	US-09-904-954-2	Sequence 2, Appli
44	179	9.7	238	3	US-09-733-756-2	Sequence 2, Appli
45	179	9.7	238	4	US-10-241-220-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1
US-10-021-121-4

Sequence 4, Application US/10021121
Publication No. US20020142444A1
GENERAL INFORMATION:

APPLICANT: Caras, Ingrid W
TITLE OF INVENTION: A2-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/021,121
FILING DATE: 06-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/635,130
FILING DATE: 19-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy B.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9981
TELEPHONE: 650/952-9981
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-021-121-4

Query Match　　　　　　100.0%; Score 1850; DB 4; Length 340;
Best Local Similarity 100.0%; Pred. No. 3.3e-131;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGPPHSGPGGVRVGALLLLGVTLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MGPPHSGPGGVRVGALLLLGVTLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

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Qy   61  LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY  120

Qy  121  SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP  180

Qy  181  VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL  240

Qy  241  GVAGAGGAMCWRRRRAKPSESRHPGGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  GVAGAGGAMCWRRRRAKPSESRHPGGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG  300

Qy  301  GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYYKV  340
         ||||||||||||||||||||||||||||||||||||||||
Db  301  GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYYKV  340
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RESULT 2
US-10-723-860-4256
; Sequence 4256, Application US/10723860
; Publication No. US20040253606A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsburg, Wendy M.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
; TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
; FILE REFERENCE: 0582.0193.NPUS01
; CURRENT APPLICATION NUMBER: US/10/723,860
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 8393
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 4256
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-723-860-4256

Query Match   100.0%; Score 1850; DB 5; Length 340;
Best Local Similarity 100.0%; Pred. No. 3.5e-131;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1  MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL   60
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Db    1  MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL   60

Qy   61  LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61  LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY  120

Qy  121  SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121  SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP  180

Qy  181  VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL  240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181  VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL  240

Qy  241  GVAGAGGAMCWRRRRAKPSESRHPGGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  GVAGAGGAMCWRRRRAKPSESRHPGGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG  300

Qy  301  GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYYKV  340
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RESULT 3
US-10-698-907-16
; Sequence 16, Application US/10698907
; Publication No. US20050049194A1
; GENERAL INFORMATION:
; APPLICANT: Frisen, Jonas
; APPLICANT: Holmberg, Johan
; TITLE OF INVENTION: Use of Ephrins and Related Molecules to Regulate Cellular
; TITLE OF INVENTION: Proliferation
; FILE REFERENCE: 21882-529 UTIL
; CURRENT APPLICATION NUMBER: US/10/698,907
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/460,488
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 10/291,290
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 60/393,272
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/345,206
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 16
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-698-907-16

Query Match   100.0%; Score 1850; DB 5; Length 340;
Best Local Similarity 100.0%; Pred. No. 3.5e-131;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1  MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL   60
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Db    1  MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL   60

Qy   61  LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY  120
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Db   61  LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY  120

Qy  121  SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP  180
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Db  121  SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP  180

Qy  181  VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL  240
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Db  181  VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL  240

Qy  241  GVAGAGGAMCWRRRRAKPSESRHPGGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG  300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241  GVAGAGGAMCWRRRRAKPSESRHPGGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG  300

Qy  301  GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYYKV  340
         ||||||||||||||||||||||||||||||||||||||||
Db  301  GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYYKV  340
```

RESULT 4
US-10-138-787-3
; Sequence 3, Application US/10138787
; Publication No. US20020172984A1
; GENERAL INFORMATION:
; APPLICANT: Holland, Sacha
; APPLICANT: Mbamalu, Geraldine
; APPLICANT: Pawson, Tony
; TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
; TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
; TITLE OF INVENTION: TYROSINE KINASES
; FILE REFERENCE: 11757.23USWO
; CURRENT APPLICATION NUMBER: US/10/138,787
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/214,631
; PRIOR FILING DATE: 1999-03-12

```
;   PRIOR APPLICATION NUMBER: PCT/CA97/00473
;   PRIOR FILING DATE: 1997-07-04
;   PRIOR APPLICATION NUMBER: 60/021,272
;   PRIOR FILING DATE: 1996-07-05
;   NUMBER OF SEQ ID NOS: 13
;   SOFTWARE: Patentin Ver. 2.0
;
;   SEQ ID NO 3
;   LENGTH: 340
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-138-787-3
```

```
Query Match        99.8%;   Score 1846;  DB 4;   Length 340;
Best Local Similarity  99.7%;   Pred. No. 7e-131;
Matches 339;  Conservative   0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL  60

Qy     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy    121 SPNLWGHEFRSHHDYIYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
            ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db    121 SPNLWGHEFRSHHDYIYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy    241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
            ||||||||||||||||||||||||||||||||||||||||
Db    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
```

```
RESULT 5
US-10-417-924A-2
;   Sequence 2, Application US/10417924A
;   Publication No. US20021591BA1
;   GENERAL INFORMATION:
;   APPLICANT: Samuel Davis, et al.
;   TITLE OF INVENTION: BIOLOGICALLY ACTIVE EPH FAMILY LIGANDS
;   FILE REFERENCE: REG-3412
;   CURRENT APPLICATION NUMBER: US/10/417,924A
;   CURRENT FILING DATE: 2003-04-17
;   PRIOR APPLICATION NUMBER: 09/051,994
;   PRIOR FILING DATE: 1998-04-24
;   PRIOR APPLICATION NUMBER: PCT/US96/17201
;   PRIOR FILING DATE: 1996-10-25
;   PRIOR APPLICATION NUMBER: 60/007,015
;   PRIOR FILING DATE: 1995-10-25
;   NUMBER OF SEQ ID NOS: 3
;   SOFTWARE: Patentin Ver. 2.0
;
;   SEQ ID NO 2
;   LENGTH: 340
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: Misc. feature
;   LOCATION: (166)
;   OTHER INFORMATION: Xaa = unknown or other
US-10-417-924A-2
```

```
Query Match        99.7%;   Score 1844;  DB 4;   Length 340;
Best Local Similarity  99.7%;   Pred. No. 9.9e-131;
Matches 339;  Conservative   0;  Mismatches  1;  Indels  0;  Gaps  0;
```

```
RESULT 6
US-10-021-121-2
;   Sequence 2, Application US/10021121
;   Publication No. US20020142444A1
;   GENERAL INFORMATION:
;   APPLICANT: Caras, Ingrid W
;   TITLE OF INVENTION: A2-1 Neurotrophic Factor
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 1 DNA Way
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatin (Genentech)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/021,121
;   FILING DATE: 06-Dec-2001
;   CLASSIFICATION: <Unknown>
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Torchia, PhD., Timothy E.
;   REGISTRATION NUMBER: 36,700
;   REFERENCE/DOCKET NUMBER: P1001
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650/225-8674
;   TELEFAX: 650/952-9981
;   INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 455 amino acids
;   TYPE: Amino Acid
;   TOPOLOGY: Linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-021-121-2
```

```
Query Match        99.5%;   Score 1841;  DB 4;   Length 455;
Best Local Similarity 100.0%;   Pred. No. 2.3e-130;
Matches 338;  Conservative   0;  Mismatches  0;  Indels  0;  Gaps  0;
```

```
Qy      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL  60

Qy     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy    121 SPNLWGHEFRSHHDYIYIIATSDGTREGLESLQGGVCLTRGMKVLLXVGQSPRGGAVPRKP 180
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    121 SPNLWGHEFRSHHDYIYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy    241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
            ||||||||||||||||||||||||||||||||||||||||
Db    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340

Qy      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

RESULT 7
US-10-698-907-8
; Sequence 8, Application US/10698907
; Publication No. US20050049194A1
; GENERAL INFORMATION:
; APPLICANT: Frisen, Jonas
; APPLICANT: Holmberg, Johan
; TITLE OF INVENTION: Use of Ephrins and Related Molecules to Regulate Cellular
; TITLE OF INVENTION: Proliferation
; FILE REFERENCE: 21882-529 UTIL
; CURRENT APPLICATION NUMBER: US/10/698,907
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/460,488
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 10/291,290
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 60/393,272
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/345,206
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 8
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-698-907-8

Query Match   96.2%; Score 1780; DB 5; Length 340;
Best Local Similarity   95.6%; Pred. No. 6.6e-126;
Matches   325; Conservative   7; Mismatches   8; Indels   0; Gaps   0;

Qy   1 MGPPHSGPGGVRVGALLLGVLGLVSGLSLEPVVWNSANKRFQAEGGYVLYPQIGDRLDL 60
              ||||| |:|||||| ||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGAPHFGPGQVGALLLGVLGLVSGLSLEPVVWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy   61 LCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFIKFQEY 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFIKFQEY 120

Qy   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy   181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAGAGLALLLL 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||:||||||
Db   181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAGMALLLL 240

Qy   241 GVAGAGGAMCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GVAGAGGAMCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy   301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYY 338
              ||||||||||||||||||||||||||||||||||||||
Db   301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYY 338

RESULT 8
US-10-408-765A-2695
; Sequence 2695, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Faby, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2695
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2695

Query Match   84.3%; Score 1559; DB 4; Length 285;
Best Local Similarity 100.0%; Pred. No. 2.4e-109;
Matches   285; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   56 DRLDLLCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTI 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 DRLDLLCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTI 60

Qy   116 KFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGA 175
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 KFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGA 120

Qy   176 VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAGAGGL 235
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL 180

Qy   236 ALLLLGVAGAGGAMCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGI 295
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 ALLLLGVAGAGGAMCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGI 240

Qy   296 ALRGGGAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYYKV 340
              |||||||||||||||||||||||||||||||||||||||||||||
Db   241 ALRGGGAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYYKV 285

Db   241 GVAGAGGAMCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Db   301 GTADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYYKV 340

RESULT 9
US-10-698-907-7
; Sequence 7, Application US/10698907
; Publication No. US20050049194A1
; GENERAL INFORMATION:
; APPLICANT: Frisen, Jonas
; APPLICANT: Holmberg, Johan
; TITLE OF INVENTION: Use of Ephrins and Related Molecules to Regulate Cellular
; TITLE OF INVENTION: Proliferation
; FILE REFERENCE: 21882-529 UTIL
; CURRENT APPLICATION NUMBER: US/10/698,907
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/460,488
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 10/291,290
; PRIOR FILING DATE: 2002-11-08

```
;  PRIOR APPLICATION NUMBER: US 60/393,272
;  PRIOR FILING DATE: 2002-07-02
;  PRIOR APPLICATION NUMBER: US 60/345,206
;  PRIOR FILING DATE: 2001-11-09
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: Patentin version 3.2
;
;  SEQ ID NO 7
;  LENGTH: 336
;  TYPE: PRT
;  ORGANISM: Mus musculus
;
US-10-698-907-7

Query Match      34.5%;  Score 637.5;  DB 5;  Length 336;
Best Local Similarity  42.1%;  Pred. No. 8e-40;
Matches 139;  Conservative 49;  Mismatches 129;  Indels 13;  Gaps 5;

Qy   14 GALLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGHSS 73
            |:||  |||| :||||||||||||||||||:||:|||||  :|:|
Db   17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPCGLVLYPQIGDKLDIICPKV---DSKTV 73

Qy   74 PNYEFYKLIVLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFFRSHH 133
            |:| |::| : | :|| || ||||||:|:|||| |||:|||||||:|| |||| || ::|
Db   74 GQYEYVKVYMVDKDQADRCTIKKENTFLLNCARPDDQDVKFTIKFQEFSPNLWGLEFQXNK 133

Qy  134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
            ||||| ||:| ||||   |||| || ||:| ||   :
Db  134 DYYIISTSNGSLEGLDNQGGVCQTRAMKILMKVGQODASSAGSARNHGPTRRPELEAGTN 193

Qy  191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
Db  194 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVLLL 253

Qy  251 WRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPRBAEPGELGIALRGGGAADPPPFCPH 310
            |||| |:: :|| || |||||||||      |:||||||||||||||
Db  254 KYRRHRHKHSPQHTTTLSLSTLATPKRGGNN---NGSEPSDVIIPLR---TADSVFCPH 306

Qy  311 YEKVSGDYGHPYYIVQDGPPQSPPPNIYYKV 340
            |||||||||||||||:  ||||| |:|||||
Db  307 YEKVSGDYGHPYYIVQEMPPQSPANIYYKV 336
```

```
RESULT 10
US-10-021-121-9
; Sequence 9, Application US/10021121
; Publication No. US20020142444A1
; GENERAL INFORMATION:
;   APPLICANT: Caras, Ingrid W
;   TITLE OF INVENTION: A2-1 Neurotrophic Factor
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Genentech, Inc.
;     STREET: 1 DNA Way
;     CITY: South San Francisco
;     STATE: California
;     COUNTRY: USA
;     ZIP: 94080
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: WinPatin (Genentech)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/10/021,121
;     FILING DATE: 06-Dec-2001
;     CLASSIFICATION: <Unknown>
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: US/08/635,130
;     FILING DATE: 19-Mar-1996
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Torchia, PhD., Timothy E.
;     REGISTRATION NUMBER: 36,700
;     REFERENCE/DOCKET NUMBER: P1001
;   TELECOMMUNICATION INFORMATION:
```

```
;     TELEPHONE: 650/225-8674
;     TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 9:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 346 amino acids
;     TYPE: Amino Acid
;     TOPOLOGY: Linear
;   SEQUENCE DESCRIPTION: SEQ ID NO: 9:
;
US-10-021-121-9

Query Match      34.2%;  Score 632;  DB 4;  Length 346;
Best Local Similarity  39.5%;  Pred. No. 2.2e-39;
Matches 145;  Conservative 48;  Mismatches 116;  Indels 58;  Gaps 9;

Qy    8 PGGVRVGALLLLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
           || :  |  ::  |  | :|||   ||||| ||||:|:| ::| ||||||:|||:|||:
Db    4 PGGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWNSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy   62 CPRARPPGPHSSSPNYEFYKLIVLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
           |||: :| |     :|| ||:|:| : | :  ||| :|||||| ||||||:|:||||||||:
Db   64 CPRAEAGRP-----YEYVKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy  122 PNLWGHEFFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVRVGQSPRGGAVPRKPV 181
           ||: |:||  : |||||| ||:| |||||  ::||| ||:||:| :|||
Db  119 PNYMGLEFQXNKHDYYITSTSNGSLEGLENRBGGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy  182 SEMPMERDRGAAHSLE--PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
               :    |  |:|  ||||||||||||||||||||||||||||||||||||
Db  179 SRPSKEADNTVRKATQAPQSSRGSLGDSDGKHETVNQEEKSGP------GASGGSSGDPD 231

Qy  237 ------LILLGVGAGGA----------MCWRRRAKPSSSRHPGPGSFGRGGSLGL 277
              |:|||||||||          :||||| |:::|||||| |||||||||||
Db  232 GFFNSKVALFAAVGAGCVTFLLIIFLTVLLLKLRKRHRKHTQQ-----RAAALSL 282

Qy  278 ---GGGGGMGPRBAEPGELGIALRGGGAADPPPFCPHYEKVSGDYGHPYYIVQDGPPQSP 333
              |||||||||||||||||||||||||||||| |||||||||||||||||:  |||||
Db  283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPYYIVQEMPPQSP 339

Qy  334 PNIYYKV 340
           ||||||
Db  340 ANIYYKV 346
```

```
RESULT 11
US-10-356-289-2
; Sequence 2, Application US/10356289
; Publication No. US20040022767A1
; GENERAL INFORMATION:
;   APPLICANT: Lyman, Stewart D.
;   APPLICANT: Beckmann, M. Patricia
;   APPLICANT: Baum, Peter R.
;   APPLICANT: Carpenter, Melissa K.
;   TITLE OF INVENTION: NOVEL CYTOKINE DESIGNATED ELK LIGAND
;   FILE REFERENCE: GENENT.67CPDV3
;   CURRENT APPLICATION NUMBER: US/10/356,289
;   CURRENT FILING DATE: 2003-01-31
;   PRIOR APPLICATION NUMBER: US/09/039,642B
;   PRIOR FILING DATE: 1998-03-16
;   PRIOR APPLICATION NUMBER: 08/213,403
;   PRIOR FILING DATE: 1994-03-15
;   PRIOR APPLICATION NUMBER: 07/977,693
;   PRIOR FILING DATE: 1992-11-13
;   PRIOR APPLICATION NUMBER: 08/747,240
;   PRIOR FILING DATE: 1996-10-12
;   PRIOR APPLICATION NUMBER: 08/460,741
;   PRIOR FILING DATE: 1995-06-02
;   NUMBER OF SEQ ID NOS: 5
;   SOFTWARE: FastSEQ for Windows Version 4.0
;
;   SEQ ID NO 2
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;
US-10-356-289-2
```

```
RESULT 12
US-10-712-124-60
Sequence 60, Application US/10712124
Publication No. US20040146907A1
GENERAL INFORMATION:
  APPLICANT: SMITH, VICTORIA
  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING DYSPLASIA
  FILE REFERENCE: P2000R1
  CURRENT APPLICATION NUMBER: US/10/712,124
  CURRENT FILING DATE: 2003-11-13
  PRIOR APPLICATION NUMBER: US 60/425,813
  PRIOR FILING DATE: 2002-11-13
  NUMBER OF SEQ ID NOS: 123
  SEQ ID NO 60
  LENGTH: 346
  TYPE: PRT
  ORGANISM: Homo sapien
US-10-712-124-60

Query Match     34.2%;  Score 632;  DB 4;  Length 346;
Best Local Similarity   39.5%;  Pred. No. 2.2e-39;
Matches  145;  Conservative  48;  Mismatches 116;  Indels  58;  Gaps  9;

Qy    8 PGGVRVGALLLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
Db    4 PGQRWLGKWLVAMVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy   62 CPRARPPGPHSSPNYEFYKLYLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
Db   64 CPRAEAGRP------YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy  122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
Db  119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy  182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
Db  179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP------GASGGSSGDPD 231

Qy  237 ------LLLLGVAGAGGA--------------MCWRRRAKPSESRHPGPGSFGRGGSLGL 277
Db  232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ------RAAALSL 282

Qy  278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGGPPQSP 333
Db  283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIIVQEMPPQSP 339

Qy  334 PNIYYKV 340
Db  340 ANIYYKV 346


RESULT 13
US-10-789-378-30
Sequence 30, Application US/10789378
Publication No. US2005003390A1
GENERAL INFORMATION:
  APPLICANT: Axenovich, Sergey
  APPLICANT: Stull, Robert
  APPLICANT: Gelman, Marina
  APPLICANT: Chui, Kitty
  APPLICANT: Ng, Dean
  TITLE OF INVENTION: DIAGNOSTIC METHODS FOR CANCER DETECTION
  FILE REFERENCE: 5189-2
  CURRENT APPLICATION NUMBER: US/10/789,378
  CURRENT FILING DATE: 2004-02-26
  PRIOR APPLICATION NUMBER: 10/441925
  PRIOR FILING DATE: 2003-05-19
  PRIOR APPLICATION NUMBER: 60/381619
  PRIOR FILING DATE: 2002-05-17
  PRIOR APPLICATION NUMBER: 60/450886
  PRIOR FILING DATE: 2003-02-26
  NUMBER OF SEQ ID NOS: 131
  SOFTWARE: Patentin version 3.1
  SEQ ID NO 30
  LENGTH: 346
  TYPE: PRT
  ORGANISM: Homo sapiens
US-10-789-378-30

Query Match     34.2%;  Score 632;  DB 5;  Length 346;
Best Local Similarity   39.5%;  Pred. No. 2.2e-39;
Matches  145;  Conservative  48;  Mismatches 116;  Indels  58;  Gaps  9;

Qy    8 PGGVRVGALLLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
Db    4 PGQRWLGKWLVAMVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy   62 CPRARPPGPHSSPNYEFYKLYLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
Db   64 CPRAEAGRP------YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy  122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
Db  119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy  182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
Db  179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP------GASGGSSGDPD 231

Qy  237 ------LLLLGVAGAGGA--------------MCWRRRAKPSESRHPGPGSFGRGGSLGL 277
Db  232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ------RAAALSL 282

Qy  278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGGPPQSP 333
Db  283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIIVQEMPPQSP 339

Qy  334 PNIYYKV 340
Db  340 ANIYYKV 346
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RESULT 14
US-10-698-907-14
; Sequence 14, Application US/10698907
; Publication No. US2005049194A1
; GENERAL INFORMATION:
; APPLICANT: Frisen, Jonas
; APPLICANT: Holmberg, Johan
; TITLE OF INVENTION: Use of Ephrins and Related Molecules to Regulate Cellular
; TITLE OF INVENTION: Proliferation
; FILE REFERENCE: 21882-529 UTIL
; CURRENT APPLICATION NUMBER: US/10/698,907
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/460,488
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 10/291,290
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 60/393,272
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/345,206
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 14
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-698-907-14

Query Match   34.2%; Score 632; DB 5; Length 346;
Best Local Similarity 39.5%; Pred. No. 2.2e-39;
Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

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Qy    8 PGGVRGALLLLGVLGLVSGLL------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
          ||| |:.|                  |||| |:.. .|:.:|  :|:||:|| ::
Db    4 PGQRWLGKWLVAMVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy   62 CPRARPGPHSSPNYEFYKLYLYVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
          |||| |||  |||||  ||| |. .:|:|.  |||||||||||||||||||||||||:|
Db   64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy  122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
          ||: | ||:. ||||| :||:|::|||.||:|||| |. ||::: .||
Db  119 PNYMGLEFKKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy  182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAGGPLPPPSMPAVAGAGGLA---- 236
          | :::. .  .    . ||.:   | : :. : .|.| |
Db  179 SRPSKEADNTVKMATQAPGSRGSLGDSDQKHETVNQEEKSGP------GASGGSSGDPD 231

Qy  237 ------LLLLGVAGAGGA------------MCWRRRAKPSESRHPGPGSFGRGGSLGL 277
                |:|| |:||.|             :.  |.:  :
Db  232 GFFNSKVALPAAVGAGCVIFLLIIIFLTVLLKLRKHRKHTQQ----RAAALSL 282

Qy  278 ----GGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
              |||||||||||||||||||||||||:.  ||||||||||||||||||  ||||||
Db  283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339

Qy  334 PNIYYKV 340
          .||||||
Db  340 ANIYYKV 346
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RESULT 15
US-09-754-105-2
; Sequence 2, Application US/09754105
; Patent No. US2001009768A1
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas
; APPLICANT: Reddy, Pranitha
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING CYTOKINE DESIGNATED LERK-5
; FILE REFERENCE: 28232
; CURRENT APPLICATION NUMBER: US/09/754,105
; CURRENT FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 09/329,531
; PRIOR FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-754-105-2

Query Match   34.0%; Score 629.5; DB 3; Length 333;
Best Local Similarity 40.9%; Pred. No. 3.2e-39;
Matches 135; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

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Qy   14 GALLLLGVLGLVSGLLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
          | |::.|    .|: :.||| ||||:|.||..:|.||:||:||:.||.||||::   .:
Db    1 GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVIYPQIGDKLDIICPKV---DSKTV 70

Qy   74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
          .:|| ||.. |.:.  ||:.  :  ||||:|::||:|::|||||||: ||||| ||:.:
Db   71 GQYETYKVZMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEBFSPNLWGLEFQRNK 130

Qy  134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
          |||| :||.|.:|||:..:|||||.||.||:|::|||  :  ..  .  : :   .
Db  131 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy  191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
          | ::.  | :. |   : .: :..|:  . |  |.: : ..  .:|:::  |.|.|.
Db  191 GRSSTTSPFVKPNFGSSTDGNSAGHSGNNILGSEVALFRAGIASGCIIFIVIIIFLVLLL 250

Qy  251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
           .||.: :|.   .  :..:.   :..     |:: .    . :..::   ||. ||
Db  251 KYRRHRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303

Qy  311 YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
          ||||||||||||:|||: ||||| |||||
Db  304 YEKVSGDYGHPVIVQEMPPQSPANIYYKV 333
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Search completed: December 21, 2005, 14:41:51
Job time : 96.7987 secs

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OM protein - protein search, using sw model

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                    GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:             December 21, 2005, 14:36:40 ; Search time 6.41509 Seconds
                                                  (without alignments)
                                                  378.002 Million cell updates/sec

Title:              US-10-021-121-4
Perfect Score:      1850
Sequence:           1 MGPPHSGPGGVRGALILLLG............PVVIVQDGPPQSPNIYYKV 340

Scoring table:      BLOSUM62
Gap op:             Gapop 10.0 , Gapext 0.5

Searched:           53982 seqs, 7132107 residues

Total number of hits satisfying chosen parameters:          53982

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing:    Minimum Match 0%
                    Maximum Match 100%
                    Listing first 45 summaries

Database :          Published Applications_AA_New:*
                    1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                    2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                    3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                    4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                    5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                    6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                    7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                    8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

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Result         %      Query
No.    Score   Match  Length  DB  ID                      Description
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  1    629.5   34.0   333     6   US-10-949-720-396       Sequence 396, App
  2    446.5   24.1   459     6   US-10-949-720-390       Sequence 390, App
  3    442     23.9   233     6   US-10-949-720-388       Sequence 388, App
  4    164.5    8.9   204     6   US-10-131-826A-288      Sequence 288, App
  5    144.5    7.8   1516    6   US-10-220-824-8         Sequence 8, Appli
  6    142.5    7.7   1496    6   US-11-186-284-35        Sequence 35, Appl
  7    142      7.7   744     7   US-11-186-284-37        Sequence 37, Appl
  8    142      7.7   744     7   US-11-186-284-39        Sequence 39, Appl
  9    141.5    7.6   1166    6   US-11-186-284-964       Sequence 964, Appl
 10    141.5    7.6   1166    7   US-10-821-234-33        Sequence 33, Appl
 11    141.5    7.6   1874    6   US-10-821-234-1182      Sequence 1182, Ap
 12    137.5    7.4   1532    6   US-10-821-234-914       Sequence 914, App
 13    135.5    7.3   1532    6   US-10-821-234-1431      Sequence 1431, Ap
 14    134.5    7.3   1366    6   US-11-186-284-31        Sequence 31, Appl
 15    133      7.2   1464    7   US-11-186-284-28        Sequence 28, Appl
 16    133      7.2   1467    6   US-11-821-234-1096      Sequence 1096, Ap
 17    132      7.1   1464    7   US-11-000-463-243       Sequence 243, Appl
 18    129      7.0   1767    6   US-10-995-561-911       Sequence 911, App
 19    129      7.0   1767    6   US-10-995-561-914       Sequence 914, App
 20    129      7.0   1806    6   US-10-995-561-912       Sequence 912, App
 21    129      7.0   1806    6   US-10-995-561-915       Sequence 915, App
 22    129      7.0   1818    6   US-10-995-561-910       Sequence 910, App
 23    129      7.0   1818    6   US-10-995-561-913       Sequence 913, App
 24    126.5    6.8   520     6   US-11-186-284-532       Sequence 532, App
 25    123      6.6   3063    7   US-11-186-284-26        Sequence 26, Appl
 26    116.5    6.3   1823    6   US-10-995-561-988       Sequence 988, App
 27    116.5    6.3   2102    6   US-10-995-561-990       Sequence 990, App
 28    116.5    6.3   2108    6   US-10-995-561-989       Sequence 989, App
 29    116.5    6.3   2157    6   US-10-995-561-991       Sequence 991, App
 30    114      6.2   828     6   US-10-995-561-983       Sequence 983, App
 31    114      6.2   918     6   US-10-995-561-981       Sequence 981, App
 32    114      6.2   1019    6   US-10-995-561-982       Sequence 982, App
 33    113.5    6.1   918     6   US-10-995-561-987       Sequence 987, App
 34    112      6.1   924     6   US-10-857-780-20        Sequence 20, Appl
 35    112      6.1   924     6   US-10-848-976-1         Sequence 1, Appl
 36    111      6.0   641     6   US-11-107-028-26        Sequence 26, Appl
 37    107      5.8   924     7   US-10-477-507A-4        Sequence 4, Appl
 38    104.5    5.6   244     6   US-10-477-507A-2        Sequence 2, Appli
 39    104.5    5.6   456     6   US-10-821-234-1688      Sequence 1688, Ap
 40    103.5    5.5   467     6   US-10-995-561-786       Sequence 786, Ap
 41    102      5.5   884     6   US-11-110-424-4         Sequence 4, Appli
 42    101.5    5.5   119     7   US-11-102-240-16        Sequence 16, Appli
 43    99.5     5.4   673     7   US-11-085-775-3         Sequence 3, Appli
 44    99       5.4   368     7   US-10-802-796-727       Sequence 727, App
 45    99       5.4   318     6   US-10-802-796-728       Sequence 728, App
                     334     6   US-10-802-796-728
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ALIGNMENTS

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RESULT 1
US-10-949-720-396
; Sequence 396, Application US/10949720
; Publication No. US20050249736A1
; GENERAL INFORMATION:
;  APPLICANT: Krasnoperov, Valery
;  APPLICANT: Zozulya, Sergey
;  APPLICANT: Kerteez, Nathalie
;  APPLICANT: Reddy, Ramachandra
;  APPLICANT: Gill, Parkash
;  TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
;  TITLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH
;  FILE REFERENCE: VASG-P02-002
;  CURRENT APPLICATION NUMBER: US/10/949,720
;  CURRENT FILING DATE: 2004-09-23
;  PRIOR APPLICATION NUMBER: US 60/454,432
;  PRIOR FILING DATE: 2003-03-12
;  PRIOR APPLICATION NUMBER: US 60/454,300
;  PRIOR FILING DATE: 2003-03-12
;  PRIOR APPLICATION NUMBER: US 10/800,350
;  PRIOR FILING DATE: 2004-03-12
;  NUMBER OF SEQ ID NOS: 425
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 396
;  LENGTH: 333
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-949-720-396

  Query Match             34.0%;  Score 629.5;  DB 6;  Length 333;
  Best Local Similarity   40.9%;  Pred. No. 1.7e-42;
  Matches  135;  Conservative  52;  Mismatches 130;  Indels 13;  Gaps 5;

Qy    14  GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPGPHSS   73
          ||:|   ||||| | ||||||||||||||  |:||||||||||||||:|:||::|:||
Db    14  GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV   70

Qy    74  PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH  133
          |:|:|:||:|:|    |  |   || |  | |  |  |  ||||||||||||||||||||
Db    71  GQYEYKVKVMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK  130

Qy   134  DYYIIATSPGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPER-DR  190
          :|| | | |  |  | | | ||   |: :||| |:    :         :: ::|  |
Db   131  DYYIISTNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN  190

Qy   191  GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAGAGGLALLLLGVAGAGAMC  250
          :  ||  | |||||  || ||:||| ||| ||||| | |:| | || ||| :::   :
Db   191  GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL  250
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Qy  251  WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPRRAEPGELGIALRGGGAADPPPFCPH  310
              ||||||   :::...                              |||
Db  251  KYRRRHRHSPQHTTLSLSTLAIPKRSGNN----NGSEPSDIIIPLR---TADSVPCPH   303

Qy  311  YEKVSGDYGHPVYIVQDGPPPQSPPNIYYKV  340
         ||||||||||    :: :|||
Db  304  YEKVSGDYGHPVYIVQEMPPQSPANIYYKV   333
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RESULT 2
US-10-949-720-390
; Sequence 390, Application US/10949720
; Publication No. US2005024973GA1
; GENERAL INFORMATION:
;   APPLICANT: Krasnoperov, Valery
;   APPLICANT: Zozulya, Sergey
;   APPLICANT: Kertesz, Nathalie
;   APPLICANT: Reddy, Ramachandra
;   APPLICANT: Gill, Parkash
;   TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
;   TITLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH
;   FILE REFERENCE: VASG-P02-002
;   CURRENT APPLICATION NUMBER: US/10/949,720
;   CURRENT FILING DATE: 2004-09-23
;   PRIOR APPLICATION NUMBER: US 60/454,432
;   PRIOR FILING DATE: 2003-03-12
;   PRIOR APPLICATION NUMBER: US 60/454,300
;   PRIOR FILING DATE: 2003-03-12
;   PRIOR APPLICATION NUMBER: US 60/454,300
;   PRIOR FILING DATE: 2003-03-12
;   PRIOR APPLICATION NUMBER: US 10/800,350
;   PRIOR FILING DATE: 2004-03-12
;   NUMBER OF SEQ ID NOS: 425
;   SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 390
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Recombinant B2EC-FC protein
US-10-949-720-390

Query Match   24.1%; Score 446.5; DB 6; Length 459;
Best Local Similarity   33.7%; Pred. No. 4.5e-28;
Matches   105; Conservative 39; Mismatches 83; Indels 85; Gaps 7;

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Qy   14  GALLLLGVLGLVGSLSLEPVYWNSANKRFQAEGGYVLLYPQIGDRLDLLCPRARPPGHSS  73
             |:||     |:|  ||||:|||||:|:|:    :|    ||||||:|::|||     ::
Db   14  GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV  70

Qy   74  PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH  133
             |: |||: ::|  |:||   ||  |  ::|||:|||||||||:||||||||| || :
Db   71  GQYEYKYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK  130

Qy  134  DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAA  193
         |||| ||: |: ||| |:::|||| || |:| |:||
Db  131  DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQ-----------------         166

Qy  194  HSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGAMCWRR   253
                         :|:.|               :.|
Db  167  --------------DASSAGSTRNKDPTRRPELE------AGTNG-----            191

Qy  254  RRAKPSESRHPGPGSFGRGGSLGLGGGGMGPRREAEPGELGIALRGGGAADP--------  305
         :|:|                                    :|:
Db  192  RSSTTSPFVKPNPGSSTDGNSAGHSGNNILG-SEVDP-----EPKSCDKTHT          237

Qy  306  -PFCPHYEKVSG  316
              :|   |||
Db  238  CPCPAPELLGG   249
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RESULT 3
US-10-949-720-388
; Sequence 388, Application US/10949720
; Publication No. US2005024973GA1
; GENERAL INFORMATION:
;   APPLICANT: Krasnoperov, Valery
;   APPLICANT: Zozulya, Sergey
;   APPLICANT: Kertesz, Nathalie
;   APPLICANT: Reddy, Ramachandra
;   APPLICANT: Gill, Parkash
;   TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
;   TITLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH
;   FILE REFERENCE: VASG-P02-002
;   CURRENT APPLICATION NUMBER: US/10/949,720
;   CURRENT FILING DATE: 2004-09-23
;   PRIOR APPLICATION NUMBER: US 60/454,432
;   PRIOR FILING DATE: 2003-03-12
;   PRIOR APPLICATION NUMBER: US 60/454,300
;   PRIOR FILING DATE: 2003-03-12
;   PRIOR APPLICATION NUMBER: US 10/800,350
;   PRIOR FILING DATE: 2004-03-12
;   NUMBER OF SEQ ID NOS: 425
;   SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 388
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Recombinant B2EC protein
US-10-949-720-388

Query Match   23.9%; Score 442; DB 6; Length 233;
Best Local Similarity   35.8%; Pred. No. 4.7e-28;
Matches   97; Conservative 36; Mismatches 76; Indels 62; Gaps 4;

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Qy   14  GALLLLGVLGLVGSLSLEPVYWNSANKRFQAEGGYVLLYPQIGDRLDLLCPRARPPGHSS  73
             |:||     |:|  ||||:|||||:|:|:    :|    ||||||:|::|||     ::
Db   14  GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV  70

Qy   74  PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH  133
             |: |||: ::|  |:||   ||  |  ::|||:|||||||||:||||||||| || :
Db   71  GQYEYKYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK  130

Qy  134  DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAA  193
         |||| ||: |: ||| |:::|||| || |:| |:||
Db  131  DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQ-----------------         166

Qy  194  HSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGAMCWRR   253
                         :|:.|               :.|
Db  167  --------------DASSAGSTRNKDPTRRPELE------AGTNG-----            191

Qy  254  RRAKPSESRHPGPGSFGRGGSLGLGGGGMG  284
         :|:|
Db  192  RSSTTSPFVKPNPGSSTDGNSAGHSGNNILG  222
```

RESULT 4
US-10-131-826A-288
; Sequence 288, Application US/10131826A
; Publication No. US2005245730A1
; GENERAL INFORMATION:
;   APPLICANT: Baker, Kevin P.
;   APPLICANT: Beresini, Maureen
;   APPLICANT: DeForge, Laura
;   APPLICANT: Desnoyers, Luc
;   APPLICANT: Filvaroff, Ellen
;   APPLICANT: Gao, Wei-Qiang
;   APPLICANT: Gerritsen, Mary E.
;   APPLICANT: Goddard, Audrey
;   APPLICANT: Godowski, Paul J.
;   APPLICANT: Gurney, Austin L.
;   APPLICANT: Sherwood, Steven
;   APPLICANT: Smith, Victoria
;   APPLICANT: Stewart, Timothy A.
;   APPLICANT: Tumas, Daniel
;   APPLICANT: Watanabe, Colin K

```
;   APPLICANT: Wood,William
;   APPLICANT: Zhang, Zemin
;   TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;   TITLE OF INVENTION: ACIDS ENCODING THE SAME
;   FILE REFERENCE: P3330R1C128
;   CURRENT APPLICATION NUMBER: US/10/131,826A
;   CURRENT FILING DATE: 2002-04-24
;   PRIOR APPLICATION NUMBER: 60/049911
;   PRIOR FILING DATE: 1997-06-18
;   PRIOR APPLICATION NUMBER: 60/056974
;   PRIOR FILING DATE: 1997-08-26
;   PRIOR APPLICATION NUMBER: 60/059113
;   PRIOR FILING DATE: 1997-09-17
;   PRIOR APPLICATION NUMBER: 60/059115
;   PRIOR FILING DATE: 1997-09-17
;   PRIOR APPLICATION NUMBER: 60/059117
;   PRIOR FILING DATE: 1997-09-17
;   PRIOR APPLICATION NUMBER: 60/059184
;   PRIOR FILING DATE: 1997-09-17
;   PRIOR APPLICATION NUMBER: 60/059122
;   PRIOR FILING DATE: 1997-09-17
;   PRIOR APPLICATION NUMBER: 60/059263
;   PRIOR FILING DATE: 1997-09-18
;   PRIOR APPLICATION NUMBER: 60/059352
;   PRIOR FILING DATE: 1997-09-19
;   PRIOR APPLICATION NUMBER: 60/059588
;   PRIOR FILING DATE: 1997-09-19
;   Remaining Prior Application data removed - See File Wrapper or PALM.
;   NUMBER OF SEQ ID NOS: 550
    SEQ ID NO 288
;   LENGTH: 204
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-131-826A-288

Query Match             8.9%;  Score 164.5;  DB 6;  Length 204;
Best Local Similarity   27.7%;  Pred. No. 1.8e-06;
Matches   46;  Conservative   31;  Mismatches   74;  Indels   15;  Gaps   5;

Qy         18 LLGVLGLVSGLSLEPVVWNSANRFQAEGGGYVLYPQIGCDRLDLLCPRARPPGPHSS-PNY 76
              |||||       |   :|  |  |||:   :|  | | :|: ||:   | :||    |||::|
Db          8 LLGLCCSLAAADRHTVFWNSSNPKFRNE--DYTIHVQLNDYVDIICPHYE---DHSADAAM 63

Qy         77 EFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLL--DLRFTIKFQEYSPNLWGHEFRSHH 133
              ||||||                    |  :|   :: |||     :| :  ||| | |||
Db         64 EQYILYLVEHEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSRKFQRFTPFTLGKEFKEGH 123

Qy        134 DYYIIATSDGTRGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK 179
              ||  |              ||   | :                |:
Db        124 SYYYISKPIHQHEDR------CLRLKVTVSGKITHSPQAHDNPQE 162
```

```
;   APPLICANT: Viromed Limited
RESULT 5
US-10-220-824-8
;   Sequence 8, Application US/10220824
;   Publication No. US2005027760JA1
;   GENERAL INFORMATION:
;   APPLICANT: Viromed Limited
;   TITLE OF INVENTION: Compositions for gene therapy of rheumatoid arthritis including a
;   TITLE OF INVENTION: gene encoding an anti-angiogenic protein or parts thereof
;   FILE REFERENCE: OPF0208/PCT
;   CURRENT APPLICATION NUMBER: US/10/220,824
;   CURRENT FILING DATE: 2002-08-30
;   PRIOR APPLICATION NUMBER: KR 2001-0000691
;   PRIOR FILING DATE: 2001-01-05
;   NUMBER OF SEQ ID NOS: 16
;   SOFTWARE: Kopatentin 1.71
    SEQ ID NO 8
;   LENGTH: 1516
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-220-824-8
```

```
Query Match             7.8%;  Score 144.5;  DB 6;  Length 1516;
Best Local Similarity   23.5%;  Pred. No. 0.00062;
Matches   73;  Conservative   18;  Mismatches   82;  Indels   137;  Gaps   15;

Qy         52 PQIGCDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDL 111
              ||  |                |:||                |||      ||||          ||
Db        620 PGVGER--------------GPPGPQGPD------------------------GPPGPS--- 640

Qy        112 RFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTRRG---LESLQGGVCLTRGMKVLLRVGQ 169
              ||    | |:                   ||  | |    |  || ::|   |    |
Db        641 ------------------FR--HDKLTFIDMEGSGPGGDLEALRG------------ 665

Qy        170 SPRGGAVPRKP--VSEMPMERDRGAAAHSLE-PGKENLPGDPTSNATSRGAAEGPLPPPSMP 226
              |||| |  |      |  |:| || | : |   ||        | | :|  |  |   | :|
Db        666 -PRGFPGPPGPPGPPGVPGLPGEPGRFGVNSSDVPGPAGLPGVP------------GPPGLP 717

Qy        227 AVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPR 286
              ||   |  |||||| ||||||||||||||||||||||||||||||||:||        |  |
Db        718 GPPGPPG------------------------GAADPPFCP------------REGPGPRTGQXGSLGEAGAPGHKGS 749

Qy        287 EAEPGELGIALRGG-------GAADPPFCP----------HYEKVSGDYGHPVVIV--Q 326
              ||| |     |               |          | |  :|   :
Db        750 KGAPGPAGARGESGLAGAPGPAGPGPGPGPGLPAGFDDMEGS-GGPFWSTARSA 808

Qy        327 DGPPGSPPNI 336
              |||  |   :|
Db        809 DG-PQGPPGL 817
```

```
RESULT 6
US-11-186-284-35
;   Sequence 35, Application US/11186284
;   Publication No. US2005026449JA1
;   GENERAL INFORMATION:
;   APPLICANT: Millennium Pharmaceuticals, Inc.
;   APPLICANT: Berger, Allison
;   APPLICANT: Guillemette, Tracy L.
;   APPLICANT: Kamatkar, Shubhangi
;   APPLICANT: Schlegel, Robert
;   APPLICANT: Monahan, John E.
;   APPLICANT: Thibodeau, Stephen N.
;   APPLICANT: Burgart, Lawrence J.
;   TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
;   TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
;   TITLE OF INVENTION: THERAPY OF COLON CANCER
;   FILE REFERENCE: MPM01-029P2RNM
;   CURRENT APPLICATION NUMBER: US/11/186,284
;   CURRENT FILING DATE: 2005-07-21
;   PRIOR APPLICATION NUMBER: US/10/301,822
;   PRIOR FILING DATE: 2002-11-21
;   PRIOR APPLICATION NUMBER: US 60/339,971
;   PRIOR FILING DATE: 2002-11-21
;   PRIOR APPLICATION NUMBER: US 60/361,978
;   PRIOR FILING DATE: 2002-03-05
;   PRIOR APPLICATION NUMBER: US 60/381,988
;   PRIOR FILING DATE: 2002-05-20
;   NUMBER OF SEQ ID NOS: 228
;   SOFTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 35
;   LENGTH: 1496
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-186-284-35
```

```
Query Match             7.7%;  Score 142.5;  DB 7;  Length 1496;
Best Local Similarity   29.1%;  Pred. No. 0.00088;
Matches   55;  Conservative   15;  Mismatches   76;  Indels   43;  Gaps   9;

Qy        169 QSPRG--GAV-PRKPVSEMPMERDRGAAHSLEPGKENLPG------------DPTSNATSRGAAE 217
              |||    ||   |||| |  |:| || |  |:|| ||
Db        500 RGPRGDPGTLGPGPVGERGAPGNRGF-----PGSDGLPGPKGAQGERGPVGSSGPKGSQ 554

Qy        218 GPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPGP----GSFGRGG 273
```

RESULT 7
US-11-186-284-37
; Sequence 37, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 744
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-37

  Query Match   7.7%; Score 142; DB 7; Length 744;
  Best Local Similarity   23.5%; Pred. No. 0.00044;
  Matches   73; Conservative 16; Mismatches   96; Indels 126; Gaps 14;

Qy   67 PPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWG 126
          :|||||| : || :
Db   198 PPGPHGLPG-------------IGKPGGPGLPGQPGPK---------------------- 222

Qy   127 HEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPM 186
          : || ||:|| ||| |:
Db   223 ---GDRGPKGLPGPQG----------LRGPKGDKGFGMPGAPGVKGP------------ 256

Qy   187 ERDRGAAHSLEPGKENLPGDPTSNATS-RGAEGPLPPPSMPAVAGAAGGLALLLL----G 241
          | :| || | :
Db   257 -----PGMHGL-PGPVGLPGVGKPGVTGPPGPQGPIGVPGCVQGPPG------------ 311

Qy   242 VAGAGGAMCWRRRAKPSESRHPG--------------------------PGSFGRGGS 274
          : || : :   :| :
Db   312 IPGIG------------KPGQDGIPGQPGPPGGKGEQGLPGLPGAPGLPGIGKPGFPGPKGD 361

Qy   275 LGLGG--GGGMGPREAEPGELGIALRGGGAADP--PFCPHYEKVSGDYGHPVYIVQDGP-- 329
          |:|| : :||| :| :
Db   362 RGMGGVPGALGPR-GEKGPIGSPGIGGSPGEPGLPGIP-----GPMGPPGAIGFPGPKG 414

Qy   330 ------PQSPP 334
          || ||
Db   415 EGGIVGPQGPP 425

RESULT 8
US-11-186-284-39
; Sequence 39, Application US/11186284
; Publication No US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 744
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-39

  Query Match   7.7%; Score 142; DB 7; Length 744;
  Best Local Similarity   23.3%; Pred. No. 0.00044;
  Matches   72; Conservative 16; Mismatches   99; Indels 122; Gaps 13;

Qy   67 PPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWG 126
          :|||||| : || :
Db   198 PPGPHGLPG-------------IGKPGGPGLPGQPGPK---------------------- 222

Qy   127 HEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPM 186
          : || ||:|| ||| |:
Db   223 ---GDRGPKGLPGPQG----------LRGPKGDKGFGMPGAPGVKGP------------ 256

Qy   187 ERDRGAAHSLEPGKENLPGDPTSNATS-RGAEGPLPPPSMPAVAGAAGGLALLLL----G 241
          | :| || | :
Db   257 -----PGMHG--PGPVGLPGVGKPGVTGPPGPQGPIGVPGCVQGPPG------------ 311

Qy   242 VAGAGGAMCWRRRAKPSESRHPG--------------------------PGSFGRGGS 274
          : || : :   :| :
Db   312 IPGIG------------KPGQDGIPGQPGPPGGKGEQGLPGLPGAPGLPGIGKPGFPGPKGD 361

Qy   275 LGLGG--GGGMGPREAEPGELGIALRGGGAADP--PFCPHYEKVSGDYGHPVYIVQDGP-- 329
          |:|| : :||| :| :
Db   362 RGMGGVPGALGPR-GEKGPIGSPGIGGSPGEPGLPGIP-----GPMGPPGAIGFPGPKG 414

Qy   330 ------PQSPP 334
          || ||
Db   417 GIVGPQGPP 425

RESULT 9
US-10-821-234-964
; Sequence 964, Application US/10821234
; Publication No. US20050025114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan

;
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
;
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
;
; SEQ ID NO 964
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-964

Query Match   7.6%; Score 141.5; DB 6; Length 1166;
Best Local Similarity   28.1%; Pred. No. 0.0008;
Matches   59; Conservative   11; Mismatches   83; Indels   57; Gaps   8;

```
Qy  165 LRVGQSP------------RGGAVPRKP---------VSEMPMER---------DRGAAHSLEPGK 200
            |  |::|            |::|              |:|               ||| |: |:|
Db  697 LRGGAGPGPGGGKGAAGPGPGPGGPGAAGTPGLQGMPGERGGLGGSPGPKGDKG------EPGG 751

Qy  201 ENLPGDPPSNATSRGAEGPLPPPSMPAVAGAVG--GLALLLLGVAGAGGAMCWRRRAKPS 259
Db  752 PGADGVPGKDG--PRGPTGPIGPGPAGPQPDGKGEGGAPGLPGIPGIVAGPRGSPGERGETGPPG 810

Qy  260 ESRHPG-----------PGSFGRGGSLGLGLGGGGGGGMGPREAEPGELGIALRGGGGAA 303
Db  811 PAGFPGAPGCQNGEPGGKGKGERGAPGEKGEGGPPGVAGPGPGKDGTSGHPGPIG------ 861

Qy  304 DPPFCHYEKVSGDYGHPVYIVQDGPPQSP 333
Db  862 -PPGPRGNRGERGSEGSPGHPGQPGPGPP 890
```

RESULT 10
US-11-186-284-33
Sequence 33, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER.
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 33
; LENGTH: 1466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-284-33

Query Match   7.6%; Score 141.5; DB 7; Length 1466;
Best Local Similarity   27.6%; Pred. No. 0.001;
Matches   61; Conservative   13; Mismatches   74; Indels   73; Gaps   10;

```
Qy  171 PRGGAVPRKPVSEMPMERDRGA----------AHSLEPGKENLPGDPTSNAT--------SRGAEG 218
Db  844 PPGGSGPAGPPGPQGVKGERGSPGGPGAAGPPGPGARGLPGPPGSNGNPGPPGPSGPSGPGKDG 903

Qy  219 PLPP-------PSMPAVAGAAGGL------------------ALLLLGVAGAGGAMCWRRRA 256
Db  904 PPGPAGNTGAPGSPGVSGPKGDAGQPGEKGSSPGAQGPPGAPGPLIGTAGITGARGLAGPPG 963

Qy  257 KPSESRHPGP-----GSFGRGGSLGLGG-GGGMGP----------------REAEPGELGIAL 297
Db  964 MPGPRGSPGPQGVKGESGKFCGANGLSGERGPPGPQGLLPGLAGTAGEPGRDGNPGSDGLPG 1023

Qy  298 RGG------------GAADPPFCPHYEKVSGDYGHPVYIVQDGPP 330
Db 1024 RDGSPGGKGDRGENGSPGAP------------GAPGHP-----GPP 1052
```

RESULT 11
US-10-821-234-1182
Sequence 1182, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
;
; SEQ ID NO 1182
; LENGTH: 1874
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1182

Query Match   7.4%; Score 137.5; DB 6; Length 1874;
Best Local Similarity   25.5%; Pred. No. 0.0028;
Matches   79; Conservative   15; Mismatches   85; Indels 131; Gaps   18;

```
Qy   61 LCPRARPPGPGHSSSPNYEFYKLYLVCGQAQG----------RRCEAPPAPNLLLTCDRPDLD 110
Db  602 LTGRPGPVGPPGS----------------CGLKGPEPGDVGPQGPRGVQGPGP---AGKP--- 642

Qy  111 LRFTIKPQEYSPNLWGHEFRSHHDYYIIIATSDGTR-----------------EGLESLQGGVC 156
Db  643 -----------GRRGR------AGSDGARGMGPGCQTGPKGDRGDGFDGLAGLPG--- 676

Qy  157 LTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGA 216
Db  677 -----------EKGHRGDPGPSGPGPPGDDGERG--DDGEVGPRGLPGP--------GPRGL 719

Qy  217 EGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRAKPSESRHPG-PGSPGRGGSL 275
Db  720 LGPKGPGPPGPPGPVTG----MDGQPGPKGNV------------GPQGBPGPGPGQQGNPGAQ 765

Qy  276 GL-GGGGGGMGPREAEPGELGIALRGG-----------------GAADPPFCPHYEKVSGDYGHPVYIVQDGP 329
Db  766 GLPGPQGAIGP----------PGEKGPLGKPGLPGMPGADGPP------------------GHP---GKEG 806

Qy  330 P-----QSPP 334
Db  807 PGEKGGQGPP 816
```

RESULT 12
US-10-821-234-914
; Sequence 914, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 914
; LENGTH: 1532
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-914

  Query Match   7.3%;   Score 135.5; DB 6;   Length 1532;
  Best Local Similarity   23.5%; Pred. No. 0.0032;
  Matches   69; Conservative   18; Mismatches 102; Indels 105; Gaps   11;

Qy   65 ARPPGPHSSPNYEFYKLYLVGGAQGRR-----------CEAPPAPNLLLTCDRPDLDRFTIKF 117
             ||||| |:|: | | |||
Db   684 AGEPGPHGPPG-----VPGSVGPKGSSGSSGSPGPGPGP------------------------ 716

Qy   118 QEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVP 177
                             ||||||||:| | ||
Db   717 ----------------VGLQGLRGEVGLP-GVK-----------------GDKGPMGCP 740

Qy   178 RKPVSEMPEMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGIAL 237
              ||| : | |
Db   741 PGPKGDQGEKGPRGLTG--AVGEPGAKGAMGPAGPDGHQGPRGEQG---- 793

Qy   238 LLLGVAGAGGAMCWRRRRAKPSRSRHPG--PGSFGRGGSLGLGGGGMGPREAEPGELGTA 296
                      : | || | :| |||||||||| || |||:
Db   794 -LTGMPGI-------RGPPGPPGSGDPGKPGLTGPGQPGQGLPGTPGPRGPGIKGEPGAPGKI 843

Qy   297 LRGGGAA-------------------------DPPFCPHYEKVSGDYVGHPVVIVQDGPPQSP 333
          ||| : |||
Db   844 VTSEGGSSMLTVPGPGPPGCAMGPPGPPGPAGPGPAGPAGGLPGHQEVLNLQGPPGPP 897

RESULT 13
US-10-821-234-1431
; Sequence 1431, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1431
; LENGTH: 1366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1431

  Query Match   7.3%;   Score 134.5; DB 6;   Length 1366;
  Best Local Similarity   25.3%; Pred. No. 0.0033;

Matches   89; Conservative   14; Mismatches 114; Indels 135; Gaps   22;

Qy   3 PPHSGPGGV--RVGALLLLGVLGLVSGLSLEPVTWNSANKRFQAEGGYVLYPQIGDRLDL 60
            ||| |:|: ||:
Db   3 PGLPGPRGIPGPVGAAGATGARGLVGEPGPAGSKGESGNKGEPGSAG-----------369

Qy   61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRR-----------CEAPPAPNLLLTCDRPDLDRF 113
          |||| |:|:
Db   321 ----GPGP-----------------------SGEBGKRGPNGEAGSAGPPGP--------- 369

; Qy   89; Conservative   14; Mismatches 114; Indels 135; Gaps   22;

RESULT 14
US-11-186-284-31
; Sequence 31, Application US/11186284
; Publication No. US20050264493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-02P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-284-31

  Query Match   7.3%;   Score 134.5; DB 7;   Length 1366;
  Best Local Similarity   25.3%; Pred. No. 0.0033;
  Matches   89; Conservative   14; Mismatches 114; Indels 135; Gaps   22;

Qy   3 PPHSGPGGV--RVGALLLLGVLGLVSGLSLEPVTWNSANKRFQAEGGYVLYPQIGDRLDL 60
            ||| |:|: ||:
Db   3 PGLPGPRGIPGPVGAAGATGARGLVGEPGPAGSKGESGNKGEPGSAG-----------369

Qy   61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRR-----------CEAPPAPNLLLTCDRPDLDRF 113
          |||| |:|:
Db   321 ----GPGP-----------------------SGEBGKRGPNGEAGSAGPPGP--------- 369

Qy   114 TIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVG-QSPR 172
                    ||||||||:| | ||
Db   396 -----PGLRG----------SPGSR-GLPGADG-------------RAGVMGPP 420

Qy   173 GGAVPRKPVSEMPEMERDRGAAHSLEP--GKENLPGDPTSNATSRGAEGPLPPPSMPAVA 229
          || | | | | |
Db   421 GSRGASGPAGVRGPNGDAGRPG--EPGLMGPRGLPGSP-GNIGPAGKEGPV--GLPGID 474

Qy   230 GAAGGLALLLLGVAGAGGAMCWRRRRAKPSRSRHPG------------PGSFGRGGSLGLGGG-G 281
                  : | || | :| |||||||||| ||
Db   475 GRPGP-----IGPAGA--------------RGEPGNIGFPGPKGPTGDPGKNGDKGHAGLAGARG 520

Qy   282 GMGP------REAEPGELGIALRGG-----GAADPP-----FCPHYEKVSGDYGHP 321
           |: | : | | ||
Db   521 APGPDGNNGAQGPFGPGGV--QGGKGEQGPAGPGPQGLPGPSGPAGEVGKP 570

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Qy    114  TIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVG-QSPR 172
                      |:|||
Db    396  --------PGLRG--------------SPGSR-GLPGADG-----------RAGVMGPP 420

Qy    173  GGAVPRKPVSEMPMERDRGAAHSLEP---GKENLPGDPTSNATSRGAEGPLPPPSMPAVA 229
                                            : |:
Db    421  GSRGASGPAGVRGPNGDAGRPG--EPGLMGPRGLPGSP-GNIGPAGKEGPV--GLPGID 474

Qy    230  GAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPG--------PGSFGRGGSLGLGGG-G 281
                                                        |:::::||:|:
Db    475  GRPGP-----IGPAGA----------RGBPQNIGFPGPGKGPTGDPGKNGDKGHAGLAGARG 520

Qy    282  GMGP-------REAEPGELGIALRGG----GAADPP---FCPHYEKVSGDYGHP 321
                :                            ::    :|:|:|
Db    521  APGPDGNGAQGPPGPQGV--QGGKGEQGPAGPGPGFQGLLPGPSGPAGEVGKP 570
```

```
Qy    205  GDPTSNATSRGAEGPLPPPSMPAVAGAAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHP 264
                                               |:|  |:
Db   1031  G-----AKGDRGETGPAGPGPAGPGAPGGAPGP----VGPAGKSG--------DRGET 1069

Qy    265  GP-GSFGRGGSLGL-GGGGGMGPR-------EAEPGELGIALRGG------GAADPPFCPHYE 312
                |                       ::|:|:
Db   1070  GPAGPAGPVGPVGARGPAGPQGPRGDKGETGEQGDRGIKGHRGFSGLQGPGPPGSSPGEQ 1129

Qy    313  KVSGDYGHPVIVQDGP--PQSPP 334
                :::  |:|:|
Db   1130  GPSG-------ASGPAGPRGPP 1144
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Qy      2  GPPHSGPGGVRVGALLLGVLGLVSGLSLEPVWNSANKRFQAEGGYVLLYPQIGDRLDLL 61
                |||          :|
Db      2  GPP--GPIG-NVGAPGAKGARG-----SAGP-----PGATGPPGAAGRVGPP 886

Qy     62  CP--RARPPGPHSSPNYEFYKLIVLVGGAQGRRCE----------APPAPNLLLTCDR 106
                |||
Db    848  GPSGNAGPPGPPGPAGKE----------GGKGPRGETGPAGRRPGEVGPPGP------ 930

Qy    107  PDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGT--REGLESLQGGVCL----TR 159
                :|  :::|                              :|
Db    931  -----------AGEKGSPGADGP--------AGAPGTPGPQGTIAGORGVVGLPGQRGER 970

Qy    160  GMKVLLRVG----QSPRGGAVPRKPVSEM---------PMERDRGAAHSLE--PGKENLP 204
                :||                                ::::
Db    971  GPPGLPGPSGPGPGPGKQGPSGASGERGPPGPMGPPGLAGPPGESGSGREGAPAAEGSPGRDGSP 1030
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RESULT 15
US-11-186-284-28

; Sequence 28, Application US/11186284
; Publication No. US20050264493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: PatentIn version 4.0
; SEQ ID NO: 28
; LENGTH: 1464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-186-284-28

Query Match   7.2%; Score 133; DB 7; Length 1464;
Best Local Similarity 25.8%; Pred. No. 0.0047;
Matches 99; Conservative 19; Mismatches 128; Indels 138; Gaps 23;

Search completed: December 21, 2005, 14:55:35
Job time : 7.41509 secs

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OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 14:25:04 ; Search time 37.2013 Seconds
(without alignments)
1011.187 Million cell updates/sec

Title: US-10-021-121-2
Perfect score: 2450
Sequence: 1 MGPPHSGPGGVRVGALLLLG..............TTLLRQRASVEAEAGQHGPL 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	Match DB	DB ID	Description
1	2450	100.0	455	2	US-08-635-130A-2	Sequence 2, Appli
2	1841	75.1	340	2	US-08-635-130A-4	Sequence 4, Appli
3	1841	75.1	340	2	US-09-949-016-6076	Sequence 6076, Ap
4	1841	75.1	397	2	US-09-949-016-10967	Sequence 10967, A
5	1837	75.0	340	2	US-09-214-631-3	Sequence 3, Appli
6	1835	74.9	340	2	US-09-051-999-2	Sequence 2, Appli
7	628.5	25.7	336	1	US-09-214-631-12	Sequence 12, Appl
8	628.5	25.7	336	1	US-08-436-044-2	Sequence 2, Appli
9	628	25.7	336	4	PCT-US95-08812-2	Sequence 2, Appli
10	623	25.4	336	2	US-08-213-403-2	Sequence 2, Appli
11	623	25.4	346	1	US-08-458-077-2	Sequence 2, Appli
12	623	25.4	346	1	US-08-460-741-2	Sequence 2, Appli
13	623	25.4	346	1	US-08-747-242-2	Sequence 2, Appli
14	623	25.4	346	2	US-08-299-567-6	Sequence 6, Appli
15	623	25.4	346	2	US-09-039-642B-2	Sequence 2, Appli
16	623	25.4	346	2	US-08-635-130A-9	Sequence 9, Appli
17	623	25.4	522	2	US-09-949-016-11189	Sequence 11189, A
18	620.5	25.3	333	1	US-08-436-054-4	Sequence 4, Appli
19	620.5	25.3	333	2	US-08-271-948-2	Sequence 2, Appli
20	620.5	25.3	333	2	US-08-739-333-2	Sequence 2, Appli
21	620.5	25.3	333	2	US-09-754-105-2	Sequence 2, Appli
22	620.5	25.3	333	2	US-09-978-339-2	Sequence 2, Appli
23	620.5	25.3	333	2	US-08-635-130A-10	Sequence 10, Appl
24	620.5	25.3	333	2	US-09-949-016-6453	Sequence 6453, Ap
25	620.5	25.3	333	4	PCT-US95-08534-2	Sequence 2, Appli
26	620.5	25.3	333	4	PCT-US95-08812-4	Sequence 4, Appli
27	620.5	25.3	333			
28	613.5	25.0	333	2	US-09-214-631-4	Sequence 4, Appli
29	599.5	24.5	345	2	US-09-214-631-5	Sequence 5, Appli
30	563.5	23.0	303	2	US-09-949-016-9295	Sequence 9295, Ap
31	489	20.0	89	2	US-09-214-631-13	Sequence 13, Appl
32	192	7.8	82	2	US-09-214-631-11	Sequence 11, Appl
33	191.5	7.8	82	2	US-09-214-631-12	Sequence 12, Appl
34	179	7.3	234	1	US-09-299-567-5	Sequence 5, Appl
35	179	7.3	238	1	US-08-240-124-2	Sequence 2, Appli
36	179	7.3	238	1	US-08-453-943-2	Sequence 2, Appli
37	179	7.3	238	2	US-08-057-121-2	Sequence 2, Appli
38	179	7.3	238	2	US-09-358-734-2	Sequence 2, Appli
39	179	7.3	238	2	US-09-949-002-378	Sequence 378, App
40	179	7.3	238	2	US-09-949-002-413	Sequence 413, App
41	179	7.3	238	2	US-09-904-954-2	Sequence 2, Appli
42	176.5	7.2	135	1	US-08-299-567-7	Sequence 7, Appli
43	176	7.2	184	2	US-08-920-440B-2	Sequence 2, Appli
44	176	7.2	184	2	US-09-173-492-2	Sequence 2, Appli
45	176	7.2	184	2	US-09-173-133-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-635-130A-2

; Sequence 2, Application US/08635130A
; Patent No. 6696557
; GENERAL INFORMATION:
; APPLICANT: Caras, Ingrid W
; TITLE OF INVENTION: A2-1 Neurotrophic Factor
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 1 DNA Way
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/635,130A
;   FILING DATE: 19-Mar-1996
;   CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;   NAME: Torchia, PhD., Timothy E.
;   REGISTRATION NUMBER: 36,700
;   REFERENCE/DOCKET NUMBER: P1001
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650/225-8674
;   TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 455 amino acids
;   TYPE: Amino Acid
;   TOPOLOGY: Linear
US-08-635-130A-2

Query Match   100.0%; Score 2450; DB 2; Length 455;
Best Local Similarity   100.0%;
Matches 455; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVTWNSANKRFQAEGGYVLYPQIGDRLDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVTWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy   61 LCPRARPPGPHSSPNYEFYKLYLYVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LCPRARPPGPHSSPNYEFYKLYLYVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

RESULT 2
US-08-635-130A-4
Sequence 4, Application US/0835130A
Patent No. 6696557

GENERAL INFORMATION:

APPLICANT: Caras, Ingrid W

TITLE OF INVENTION: A2-1 Neurotrophic Factor

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/635,130A
FILING DATE: 19-Mar-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 340 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear

US-08-635-130A-4

Query Match   75.1%;   Score 1841;   DB 2;   Length 340;
Best Local Similarity   100.0%;   Pred. No. 5.5e-148;
Matches 338;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy     1 MGPPHSGPGGVRVGALLLLGVLLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MGPPHSGPGGVRVGALLLLGVLLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy    61 LCPRARPPGPHSSPNYEFYKLYLVGGAQRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 LCPRARPPGPHSSPNYEFYKLYLVGGAQRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy   181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy   241 GVAGAGGAMCWRRRARKPSESRHPGPGSPGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GVAGAGGAMCWRRRARKPSESRHPGPGSPGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy   301 GAADPPPCPHYEKVSGDYGHPVVIVQDGPPQSPPNIIY 338
           ||||||||||||||||||||||||||||||||||||||
Db   301 GAADPPPCPHYEKVSGDYGHPVVIVQDGPPQSPPNIIY 338
```

RESULT 3
US-09-949-016-6076
Sequence 6076, Application US/09949016
Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6076

LENGTH: 340
TYPE: PRT
ORGANISM: Human

US-09-949-016-6076

Query Match   75.1%;   Score 1841;   DB 2;   Length 340;
Best Local Similarity   100.0%;   Pred. No. 5.5e-148;
Matches 338;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy     1 MGPPHSGPGGVRVGALLLLGVLLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 MGPPHSGPGGVRVGALLLLGVLLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy    61 LCPRARPPGPHSSPNYEFYKLYLVGGAQRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 LCPRARPPGPHSSPNYEFYKLYLVGGAQRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy   181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy   241 GVAGAGGAMCWRRRARKPSESRHPGPGSPGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GVAGAGGAMCWRRRARKPSESRHPGPGSPGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy   301 GAADPPPCPHYEKVSGDYGHPVVIVQDGPPQSPPNIIY 338
           ||||||||||||||||||||||||||||||||||||||
Db   301 GAADPPPCPHYEKVSGDYGHPVVIVQDGPPQSPPNIIY 338
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Qy   361 CSRVTTFLFPVQVITTSTCRMTSFSFTTLNPSMQACRAQMGEFRIRWCFWGDRILGTALF 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 VLVLILILLGRLNMHQTTLLRQRASVEAEAGQHGPL 455

Qy   361 CSRVTTFLFPVQVITTSTCRMTSFSFTTLNPSMQACRAQMGEFRIRWCFWGDRILGTALF 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   421 VLVLILILLGRLNMHQTTLLRQRASVEAEAGQHGPL 455
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RESULT 4
US-09-949-016-10967
Sequence 10967, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10967
LENGTH: 397
TYPE: PRT
ORGANISM: Human
US-09-016-10967

Query Match   75.1%; Score 1841; DB 2; Length 397;
Best Local Similarity   100.0%; Pred. No. 6.8e-148;
Matches 338; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   58 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 117

Qy   61 LCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   118 LCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 177

Qy   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   178 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 237

Qy   181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   238 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 297

Qy   241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   298 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG 357

Qy   301 GAADPPPCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              ||||||||||||||||||||||||||||||||||||||
Db   358 GAADPPPCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 395

RESULT 5
US-09-214-631-3
Sequence 3, Application US/09214631
Patent No. 6413730
GENERAL INFORMATION:
APPLICANT: Holland, Sacha
APPLICANT: Mbamalu, Geraldine
APPLICANT: Pawson, Tony
TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
TITLE OF INVENTION: TYROSINE KINASES
FILE REFERENCE: 11757.23USWO
CURRENT APPLICATION NUMBER: US/09/214,631
CURRENT FILING DATE: 1999-03-12
EARLIER APPLICATION NUMBER: PCT/CA97/00473
EARLIER FILING DATE: 1997-07-04
EARLIER APPLICATION NUMBER: 60/021,272
EARLIER FILING DATE: 1996-07-05
NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 340
TYPE: PRT
ORGANISM: Homo sapiens
US-09-214-631-3

Query Match   75.0%; Score 1837; DB 2; Length 340;
Best Local Similarity   99.7%; Pred. No. 1.2e-147;
Matches 337; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

Qy   1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy   61 LCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy   181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy   241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG 300

Qy   301 GAADPPPCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
              ||||||||||||||||||||||||||||||||||||||
Db   301 GAADPPPCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338

RESULT 6
US-09-051-994-2
Sequence 2, Application US/09051994A
Patent No. 660283
GENERAL INFORMATION:
APPLICANT: REGENERON PHARMACEUTICALS, INC.
TITLE OF INVENTION: BIOLOGICALLY ACTIVE EPH FAMILY LIGANDS
FILE REFERENCE: REG-341-PCT-US
CURRENT APPLICATION NUMBER: US/09/051,994A
CURRENT FILING DATE: 1998-04-24
EARLIER APPLICATION NUMBER: PCT/US96/17201
EARLIER FILING DATE: 1996-10-25
EARLIER APPLICATION NUMBER: 60/007,015
EARLIER FILING DATE: 1995-10-25
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 340
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: site
LOCATION: (166)
OTHER INFORMATION: Xaa=Arg or Gln
US-09-051-994-2

Query Match   74.9%; Score 1835; DB 2; Length 340;
Best Local Similarity   99.7%; Pred. No. 1.8e-147;
Matches 337; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

Qy   1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy   61 LCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

RESULT 7
US-08-436-044-2
Sequence 2, Application US/08436044
; Patent No. 5624899
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Matthews, William
; TITLE OF INVENTION: HTK LIGAND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,044
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/277722
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 90203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-436-044-2

Query Match   25.7%; Score 628.5; DB 1; Length 336;
Best Local Similarity   41.8%; Pred. No. 3.3e-45;
Matches 137; Conservative   49; Mismatches 129; Indels 13; Gaps   5;

Qy   14 GALLLLGVILGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
           ||| ||: |:| ::| ||::||||:||.|:| | |:||||||||:||::||:   ..:
Db   17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGGGLVLYPQIGDKLDIICPKV---DSKTV 73

Qy   74 PNVEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
           .|.|:||:|::. ||:||| . |.||.| |||::| :||||||:|||||||:||:..:
Db   74 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133

Qy   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLXVGQSPRGGAVPRKP 180

Qy   181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy   241 GVAGAGGAMCWRRRARKPSESRHPGGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GVAGAGGAMCWRRRARKPSESRHPGGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy   301 GAADPPPFCPHYEKVSGDYGHPVYVIVQDGPPQSPPNIYY 338
           ||||||||||||||||||||||||||||||||||||||||
Db   301 GAADPPPFCPHYEKVSGDYGHPVYVIVQDGPPQSPPNIYY 338

RESULT 8
US-08-436-054-2
Sequence 2, Application US/08436054
; Patent No. 5864020
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Matthews, William
; TITLE OF INVENTION: HTK LIGAND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,054
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/277722
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 902D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-436-054-2

Query Match   25.7%; Score 628.5; DB 1; Length 336;
Best Local Similarity   41.8%; Pred. No. 3.3e-45;
Matches 137; Conservative   49; Mismatches 129; Indels 13; Gaps   5;

Qy   14 GALLLLGVILGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
           ||| ||: |:| ::| ||::||||:||.|:| | |:||||||||:||::||:   ..:
Db   17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGGGLVLYPQIGDKLDIICPKV---DSKTV 73

Qy   74 PNVEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
           .|.|:||:|::. ||:||| . |.||.| |||::| :||||||:|||||||:||:..:
Db   74 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133

Qy   134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
           ||||| || .:.||.::| |:|||.|| |||: ||| :.. | | :| | |:||| . .:
Db   134 DYYIISTSNGSLEGLDNQGEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

Qy   191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
           | :.: |:::.||.||.||: | |..|| : . | :| | |::: | ..:| |
Db   194 GRSSTTSPFVKRNPGGSSTDGNSAGHSGNNILGGSEVALFAGIASGCCIIFIVIIILVLLI 253

Qy   251 WRRRAKPSESRHPGGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
           :| |.:.|||:..|:..: :|| ::| | : | .. : :|: | :| |.||||
Db   254 KYFRRHRKHSPQHTTTLSLSTLATPKRGGNN-----NGSEPSDVIIPLR---TADSVFCPH 306

Qy   311 YEKVSGDYGHPVYVIVQDGPPQSPPNIYY 338
           ||||||||||||||||||:. ||||.|||
Db   307 YEKVSGDYGHPVYVIVQEMPPQSPANIYY 334

RESULT 9
PCT-US95-08812-2
; Sequence 2, Application PC/TUS9508812
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: HTK LIGAND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08812
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 902PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

PCT-US95-08812-2

Query Match   25.7%;   Score 628.5;   DB 4;   Length 336;
Best Local Similarity   41.8%;   Pred. No. 3.3e-45;
Matches 137;   Conservative   49;   Mismatches 129;   Indels 13;   Gaps 5;

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Qy   14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLLDLLCPRARPPGPHSS 73
           |:||:|||||:::|:||||||||||||||||:|||||||:||::|||  |:| | |::
Db   17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73

Qy   74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLLRFTIKFQEYSPNLWGHEFRSHH 133
          :|||| |::||:||||||||| ||||:|:|||| :||||||||||:||||   :||::
Db   74 GQYEYYKYMVMDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133

Qy  134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
          ||:|||||||:|||||:||||||:|||||||||||   :||:|| |:|:|:|::  ||
Db  134 DYYIISTNGSLEGLDNQGGVCQTRAMKILMKVGQDASSAGSARNHGFTRRPELEAGTN 193
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RESULT 10
US-08-213-403-2
; Sequence 2, Application US/08213403
; Patent No. 5512457
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M Patricia
; APPLICANT: Baum, Peter R
; APPLICANT: Carpenter, Melissa
; TITLE OF INVENTION: No. 5512457el Cytokine Designated elk ligand
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/213,403
; FILING DATE: 15-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,693
; FILING DATE: 13-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-213-403-2

Query Match   25.4%;   Score 623;   DB 1;   Length 346;
Best Local Similarity   39.2%;   Pred. No. 1e-44;
Matches 143;   Conservative   48;   Mismatches 116;   Indels 58;   Gaps 9;

```
Qy    8 PGGVRVGALLLLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
           ||  |  |||||:|:|||||      ||||||||||||||:|||||||||||||||:|
Db    4 PGQRWLGKNLVAMVVWALCRLATPLAKNLEPVSWNSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy   62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLLRFTIKFQEYS 121
          ||||||||||::  :||||||||||||||||||||||||||:||||||||||||||||:
Db   64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy  122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
          ||||| |||::|||||:||:||||||:|||||||:|||||||||:||:::|||| |:|
Db  119 PNYMGLEFKHHDVYITSTSNGSLEGLENRGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178
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(Additional alignment fragment shown on page:)

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Qy  134 DYYIISTNGSLEGLDNQGGVCQTRAMKILMKVGQDASSAGSARNHGFTRRPELEAGTN 193
Db  119 PNYMGLEFKHHDVYITSTSNGSLEGLENRGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178
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Qy  191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
Db  191 GRSSTTSPFVKPNFGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIFIVIIILLVLLL 253

Qy  251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
Db  254 KYRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH 306

Qy  311 YEKVSGDYGHPVIVQDGPPQSPPNIYY 338
Db  307 YEKVSGDYGHPVIIVQEMPPQSPANIYY 334
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RESULT 11
US-08-458-077-2
; Sequence 2, Application US/08458077
; Patent No. 5627267
; GENERAL INFORMATION:
;   APPLICANT: Lyman, Stewart D.
;   APPLICANT: Beckmann, M. Patricia
;   APPLICANT: Baum, Peter R.
;   APPLICANT: Carpenter, Melissa
; TITLE OF INVENTION: No. 5627267el Cytokine Designated elk Ligand
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Immunex Corporation
;   STREET: 51 University Street
;   CITY: Seattle
;   STATE: Washington
;   COUNTRY: USA
;   ZIP: 98101
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: Apple Macintosh
;   OPERATING SYSTEM: Apple System 7.1
;   SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/458,077
;   FILING DATE: 01-JUN-1995
;   CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/213,403
;   FILING DATE: 15-MAR-1994
;   APPLICATION NUMBER: US 07/977,693
;   FILING DATE: 13-NOV-1992
;   APPLICATION NUMBER: 514
;   CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
;   NAME: Seese, Kathryn A.
;   REGISTRATION NUMBER: 32,172
;   REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (206) 587-0430
;   TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 346 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-458-077-2

Query Match   25.4%; Score 623; DB 1; Length 346;
Best Local Similarity   39.2%; Pred. No. 1e-44;
Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps   9;

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Qy    8 PGGVRVGALILLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLYPIQGDRLDLL  61
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Db    4 PGGQRWLGKWLVAMVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII  63

Qy  182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPSMPAVAGAAGGLA----  236
Db  179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-------GASGSSGDPD  231

Qy  237 --------LLLLGVAGAGGA------MCWRRRAKPSESRHPGPGSFGRGGSLGL        277
Db  232 GFFNSKVALFAAVGAGCVIFLLIIFLTVLLLKLRKRHRKHTQQ------RAAALSL      282

Qy  278 ---GGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP    333
Db  283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVIVQEMPPQSP  339

Qy  334 PNIYY  338
Db  340 ANIYY  344
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RESULT 12
US-08-460-741-2
; Sequence 2, Application US/08460741
; Patent No. 5670625
; GENERAL INFORMATION:
;   APPLICANT: Lyman, Stewart D.
;   APPLICANT: Beckmann, M. Patricia
;   APPLICANT: Baum, Peter R.
;   APPLICANT: Carpenter, Melissa
; TITLE OF INVENTION: No. 5670625el Cytokine Designated elk Ligand
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Immunex Corporation
;   STREET: 51 University Street
;   CITY: Seattle
;   STATE: Washington
;   COUNTRY: USA
;   ZIP: 98101
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: Apple Macintosh
;   OPERATING SYSTEM: Apple System 7.1
;   SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/460,741
;   FILING DATE: 02-JUN-1995
;   CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/213,403
;   FILING DATE: 15-MAR-1994
;   APPLICATION NUMBER: US 07/977,693
;   FILING DATE: 13-NOV-1992
;   CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
;   NAME: Seese, Kathryn A.
;   REGISTRATION NUMBER: 32,172
;   REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (206) 587-0430
;   TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 346 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-460-741-2

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Qy   62 CPRARPPGPHSSPNYEFYKLYLLVGGAQGRRCEAPPAPNLLLTCDRPFDLLRFTIKFQEYS  121
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Qy  122 PNLWGHERSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLLRVGQSPRGGAVPRKPV  181
Db  119 PNTWGLEFKKHHDYYIITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy  182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPSMPAVAGAAGGLA---    236
Db  179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP------GASGSSGDPD    231

Qy  237 -------LLLLGVAGAGGA------MCWRRRAKPSESRHPGPGSFGRGGSLGL         277
Db  232 GFFNSKVALFAAVGAGCVIFLLIIFLTVLLLKLRKRHRKHTQQ------RAAALSL      282

Qy  278 ---GGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP   333
Db  283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVIVQEMPPQSP  339

Qy  334 PNIYY  338
Db  340 ANIYY  344
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RESULT 13
US-08-747-240-2
; Sequence 2, Application US/08747240
; Patent No. 5728813
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; APPLICANT: Baum, Peter R
; APPLICANT: Carpenter, Melissa
; TITLE OF INVENTION: No. 5728813el Cytokine Designated elk Ligand
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Immunex Corporation
;   STREET: 51 University Street
;   CITY: Seattle
;   STATE: Washington
;   COUNTRY: USA
;   ZIP: 98101
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: Apple Macintosh
;   OPERATING SYSTEM: Apple System 7.1
;   SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/747,240
;   FILING DATE: 12-Nov-1996
;   CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/213,403
;   FILING DATE: 15-Mar-1994
;   APPLICATION NUMBER: US 07/977,693
;   FILING DATE: 13-Nov-1992
;   CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;   NAME: Seese, Kathryn A.
;   REGISTRATION NUMBER: 32,172
;   REFERENCE/DOCKET NUMBER: 2807-A
;   TELEPHONE: (206) 587-0430

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Query Match    25.4%;  Score 623;  DB 1;  Length 346;
Best Local Similarity 39.2%;  Pred. No. 1e-44;
Matches 143;  Conservative 48;  Mismatches 116;  Indels 58;  Gaps 9;

Qy    8 PGGVRVGALLLLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLIYPQIGDRLDLL 61
          ||||| :||: :| ::| |||       :|:||||||||||||||||||:|||||||:
Db    4 PGQRWLGKWLVAMVVWALCRIATPLAKNLBPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy   62 CPRARPPGPHSSPNYEFYKLYLYGGAQGRRCEAPPAPNLLLTCDRPDLDLRFFIKFQEYS 121
          ||||:||||  |:|:||||||:||||||  |  ||::|| |||||||||:||||||::|
Db   64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy  122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
          |:: |||:|||||||| ||| :||||| | ||||: |:|:|: :|||:||  :||||
Db  119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy  182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
          |  :|:||  | |||| |||:|||||||| :|||  |||||||:|||||:|||| 
Db  179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP------GASGGSSGDPD 231

Qy  237 ------LLILGVAGAGA------------MCWRRRAKPSESRHPGPGSFGRGGSLGL 277
               |:|||:||||||             |: :  ::  : ::|:
Db  232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKHRKHTQQ------RAAALSL 282

Qy  278 ----GGGGGMGPREAEPGELGIALRGGGAADPPPCPHYEKVSGDYGHPVYIVQDGPPQSP 333
          ::|:||||||||::|:||||:|||||||||||
Db  283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339

Qy  334 PNIYY 338
          ||||
Db  340 ANIYY 344
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; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 346 amino acids
;   TYPE: amino acids
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-747-240-2

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Query Match    25.4%;  Score 623;  DB 1;  Length 346;
Best Local Similarity 39.2%;  Pred. No. 1e-44;
Matches 143;  Conservative 48;  Mismatches 116;  Indels 58;  Gaps 9;

Qy    8 PGGVRVGALLLLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLIYPQIGDRLDLL 61
          ||||| :||: :| ::| |||       :|:||||||||||||||||||:|||||||:
Db    4 PGQRWLGKWLVAMVVWALCRIATPLAKNLBPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy   62 CPRARPPGPHSSPNYEFYKLYLYGGAQGRRCEAPPAPNLLLTCDRPDLDLRFFIKFQEYS 121
          ||||:||||  |:|:||||||:||||||  |  ||::|| |||||||||:||||||::|
Db   64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy  122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
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Db  119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy  182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
          |  :|:||  | |||| |||:|||||||| :|||  |||||||:|||||:|||| 
Db  179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP------GASGGSSGDPD 231

Qy  237 ------LLILGVAGAGA------------MCWRRRAKPSESRHPGPGSFGRGGSLGL 277
               |:|||:||||||             |: :  ::  : ::|:
Db  232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKHRKHTQQ------RAAALSL 282

Qy  278 ----GGGGGMGPREAEPGELGIALRGGGAADPPPCPHYEKVSGDYGHPVYIVQDGPPQSP 333
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Db  283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339

Qy  334 PNIYY 338
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Db  340 ANIYY 344
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RESULT 14
US-08-299-567-6
; Sequence 6, Application US/08299567
; Patent No. 5747033
; GENERAL INFORMATION:
; APPLICANT: Davis, et al.
; TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
; TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Regeneron Pharmaceuticals, Inc.
;   STREET: 777 Old Saw Mill River Road
;   CITY: Tarrytown
;   STATE: New York
;   COUNTRY: U.S.A.
;   ZIP: 10591-6707
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/299,567
;   FILING DATE: 01-SEP-1994
;   CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
;   NAME: Kempler, Gail M.
;   REGISTRATION NUMBER: 32,143
;   REFERENCE/DOCKET NUMBER: REG 290
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 914-345-7400

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;   TELEFAX: 914-345-7721
; INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 346 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: unknown
;   MOLECULE TYPE: protein
US-08-299-567-6

Query Match       25.4%; Score 623; DB 1; Length 346;
Best Local Similarity 39.2%; Pred. No. 1e-44;
Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

Qy    8 PGGVRVGALLLLGVLGLVSGL------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
          |||:|| | |  | |||:||        ||||| ::|:|| |  ||::||:|::|||:||:
Db    4 PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy   62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
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Db   64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy  122 PNLWGHEFRSHHDYYIIATSDGTREGLLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
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Db  119 PNYMGLEFXKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy  182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAGGLA---236
          |   :|| :    |:  ||   |  |: : ::           |  ||||| || |
Db  179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-------GASGSSSGDPD 231

Qy  237 ------LLILGVAGAGGA------MCWRRRAKPSESRHPGPGSFGRGGSLGL 277
               |:|:|||||| |         :| : |::  |: | |||| | ||
Db  232 GFFNSKVALFAAVGAGCVIFLLLIIIIFLTVLLLKLRKRHRKHTQQ------RAAALSL 282

Qy  278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
            :: | |||| | |  |  :| | ||   |:|||||||||||||||||:| ||||
Db  283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339

Qy  334 PNIYY 338
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Db  340 ANIYY 344
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RESULT 15
US-09-039-642B-2
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; Sequence 2, Application US/09039642B
; Patent No. 6540992
; GENERAL INFORMATION:
;   APPLICANT: Lyman, Stewart D.
;   APPLICANT: Beckmann, M. Patricia
;   APPLICANT: Baum, Peter R.
;   APPLICANT: Carpenter, Melissa K.
;   TITLE OF INVENTION: NOVEL CYTOKINE DESIGNATED ELK LIGAND
;   FILE REFERENCE: GENENT.67CPDV3
;   CURRENT APPLICATION NUMBER: US/09/039,642B
;   CURRENT FILING DATE: 1998-03-16
;   PRIOR APPLICATION NUMBER: 08/213,403
;   PRIOR FILING DATE: 1994-03-15
;   PRIOR APPLICATION NUMBER: 07/977,693
;   PRIOR FILING DATE: 1992-11-13
;   PRIOR APPLICATION NUMBER: 08/747,240
;   PRIOR FILING DATE: 1996-10-12
;   PRIOR APPLICATION NUMBER: 08/460,741
;   PRIOR FILING DATE: 1995-06-02
;   NUMBER OF SEQ ID NOS: 5
;   SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-039-642B-2

Query Match       25.4%; Score 623; DB 2; Length 346;
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OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: December 21, 2005, 14:30:39 ; Search time 128.201 seconds
                 (without alignments)
                 1482.921 Million cell updates/sec

Title: US-10-021-121-2
Perfect score: 2450
Sequence: 1 MGPPHSGPGGVRVGALILLG..........TTLLRQRASVEAEAGQHGPL 455
Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5
Searched: 1867569 seqs, 417829326 residues

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published Applications_AA_Main:*
                 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters: 1867569

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2450	100.0	455	4	US-10-021-121-2	Sequence 2, Appli
2	1841	75.1	340	5	US-10-021-121-4	Sequence 4, Appli
3	1841	75.1	340	5	US-10-723-860-4256	Sequence 4256, Ap
4	1837	75.1	340	5	US-10-698-907-16	Sequence 16, Appli
5	1837	75.0	340	5	US-10-138-787-3	Sequence 3, Appli
6	1835	74.9	340	5	US-10-417-924A-2	Sequence 2, Appli
7	1771	72.3	340	5	US-10-698-907-8	Sequence 8, Appli
8	1550	63.3	285	4	US-10-408-765A-2695	Sequence 2695, Ap
9	628.5	25.7	336	5	US-10-698-907-7	Sequence 7, Appli
10	623	25.4	346	4	US-10-021-121-9	Sequence 9, Appli
11	623	25.4	346	4	US-10-356-289-2	Sequence 2, Appli
12	623	25.4	346	5	US-10-711-124-60	Sequence 60, Appli
13	623	25.4	346	5	US-10-789-378-30	Sequence 30, Appli
14	623	25.3	346	5	US-10-698-907-14	Sequence 14, Appli
15	620.5	25.3	333	3	US-09-754-105-2	Sequence 2, Appli
16	620.5	25.3	333	5	US-09-978-339-2	Sequence 2, Appli
17	620.5	25.3	333	4	US-10-021-121-10	Sequence 10, Appli
18	620.5	25.3	333	4	US-10-331-496A-63	Sequence 63, Appli
19	620.5	25.3	333	4	US-10-698-639-62	Sequence 62, Appli
20	620.5	25.3	333	5	US-10-698-907-15	Sequence 15, Appli
21	620.5	25.3	333	5	US-10-800-350-396	Sequence 396, App
22	620.5	25.0	333	4	US-10-800-077-396	Sequence 396, App
23	613.5	25.0	333	4	US-10-138-787-4	Sequence 4, Appli
24	604.5	24.7	345	5	US-10-699-907-5	Sequence 5, Appli
25	599.5	24.5	345	4	US-10-138-787-5	Sequence 5, Appli
26	489	20.0	89	4	US-09-862-179A-17	Sequence 17, Appl
27	489	20.0	89	4	US-10-138-787-13	Sequence 13, Appl
28	451.5	18.4	459	5	US-10-800-350-390	Sequence 390, App
29	451.5	18.4	459	5	US-10-800-077-390	Sequence 390, App
30	447	18.2	229	5	US-10-698-907-20	Sequence 20, Appl
31	443	18.1	226	5	US-10-698-907-21	Sequence 21, Appl
32	442	18.0	233	5	US-10-800-350-388	Sequence 388, App
33	442	18.0	233	5	US-10-800-077-388	Sequence 388, App
34	284.5	11.6	92	5	US-09-864-761-48262	Sequence 48262, A
35	196.5	8.0	136	3	US-09-864-761-48257	Sequence 48257, A
36	193.5	7.9	106	3	US-09-925-297-639	Sequence 639, App
37	192	7.8	82	3	US-09-862-179A-15	Sequence 15, Appl
38	192	7.8	82	4	US-10-138-787-11	Sequence 11, Appl
39	192	7.8	652	6	US-11-097-143-2655	Sequence 2655, Ap
40	192	7.8	652	6	US-11-097-143-23436	Sequence 23436, A
41	191.5	7.8	82	3	US-09-862-179A-16	Sequence 16, Appl
42	191.5	7.8	82	4	US-10-138-787-12	Sequence 12, Appl
43	179	7.3	238	4	US-09-904-954-2	Sequence 2, Appli
44	179	7.3	238	3	US-09-733-756-2	Sequence 2, Appli
45	179	7.3	238	4	US-10-241-220-72	Sequence 72, Appl

ALIGNMENTS

RESULT 1
US-10-021-121-2
Sequence 2, Application US/10021121
Publication No. US20020142444A1
GENERAL INFORMATION:

APPLICANT: Caras, Ingrid W
TITLE OF INVENTION: A2-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/021,121
FILING DATE: 06-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/635,130
FILING DATE: 19-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 455 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-021-121-2

Query Match 100.0%; Score 2450; DB 4; Length 455;
Best Local Similarity 100.0%; Pred. No. 1.6e-179;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGPPHSGPGGVRVGALILLLGVLGVSGLSLEPVTWNSANKRFQAEGGYVLYPQIGDRLDL 60
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Db 1 MGPPHSGPGGVRVGALILLLGVLGVSGLSLEPVTWNSANKRFQAEGGYVLYPQIGDRLDL 60

RESULT 2
US-10-021-121-4
Sequence 4, Application US/10021121
Publication No. US20020142444A1
GENERAL INFORMATION:
APPLICANT: Caras, Ingrid W
TITLE OF INVENTION: A2-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/021,121
FILING DATE: 06-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/635,130
FILING DATE: 19-Mar-1996
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 340 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-021-121-4

Query Match   75.1%;   Score 1841; DB 4; Length 340;
Best Local Similarity 100.0%;   Pred. No. 6.4e-133;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  61  LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY  120
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Db  61  LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY  120

Qy 121  SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP  180
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Db 121  SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP  180

Qy 181  VSEMPMERDRGAAHSLEPGKENLPGDPTPSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL  240
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Db 181  VSEMPMERDRGAAHSLEPGKENLPGDPTPSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL  240

Qy 241  GVAGAGGAMCWRRRARAKFSESRHPGGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG  300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241  GVAGAGGAMCWRRRARAKFSESRHPGGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG  300

Qy 301  GAADPPPFCPHYEKVSGDYGHPVYIVQDGPPQSSPPNIYYTSISVLEWPILHTIQLFFMRSK  360
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Db 301  GAADPPPFCPHYEKVSGDYGHPVYIVQDGPPQSSPPNIYYTSISVLEWPILHTIQLFFMRSK  360

Qy 361  CSRVTTLFPVQVITTSTCRMTSFSFTTLNPSMQACRAQMGEFRIRWCFWGDRILGTALF  420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 361  CSRVTTLFPVQVITTSTCRMTSFSFTTLNPSMQACRAQMGEFRIRWCFWGDRILGTALF  420

Qy 421  VLVLILLLGRLNMHQTTLLRQRASVEABAGQHGPL  455
        |||||||||||||||||||||||||||||||||||
Db 421  VLVLILLLGRLNMHQTTLLRQRASVEABAGQHGPL  455
```

RESULT 3
US-10-723-860-4256
Sequence 4256, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUS01
CURRENT FILING DATE: 2003-11-26
CURRENT APPLICATION NUMBER: US/10/723,860
PRIOR FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: 60/429,739
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: Patentin version 3.2
SEQ ID NO 4256
LENGTH: 340
TYPE: PRT
ORGANISM: Homo sapiens
US-10-723-860-4256

Query Match   75.1%;   Score 1841; DB 5; Length 340;
Best Local Similarity 100.0%;   Pred. No. 6.4e-133;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy   1  MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1  MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL  60

Qy  61  LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY  120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61  LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY  120

Qy 121  SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP  180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 121  SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP  180

Qy 181  VSEMPMERDRGAAHSLEPGKENLPGDPTPSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL  240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 181  VSEMPMERDRGAAHSLEPGKENLPGDPTPSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL  240

Qy 241  GVAGAGGAMCWRRRARAKFSESRHPGGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG  300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 241  GVAGAGGAMCWRRRARAKFSESRHPGGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG  300

Qy 301  GAADPPPFCPHYEKVSGDYGHPVYIVQDGPPQSSPPNIYY  338
        ||||||||||||||||||||||||||||||||||||||||
Db 301  GAADPPPFCPHYEKVSGDYGHPVYIVQDGPPQSSPPNIYY  338
```

```
Qy  301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
        ||||||||||||||||||||||  |||||||||||||||
Db  301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYY 338
```

RESULT 4
US-10-698-907-16
; Sequence 16, Application US/10/698907
; Publication No. US2005004919A1
; GENERAL INFORMATION:
; APPLICANT: Frisen, Jonas
; APPLICANT: Holmberg, Johan
; TITLE OF INVENTION: Use of Ephrins and Related Molecules to Regulate Cellular
; TITLE OF INVENTION: Proliferation
; FILE REFERENCE: 21882-529 UTIL
; CURRENT APPLICATION NUMBER: US/10/698,907
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/460,488
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 10/291,290
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 60/393,272
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/345,206
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 16
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-698-907-16

  Query Match   75.1%; Score 1841; DB 5; Length 340;
  Best Local Similarity   100.0%; Pred. No. 6.4e-133;
  Matches 338; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy    1 MGPPHSGPGGVRVGALLLLGVLGVLSGLSLEPVYWNSANKRFQAEGGYVYLYPQIGDRLDL 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MGPPHSGPGGVRVGALLLLGVLGVLSGLSLEPVYWNSANKRFQAEGGYVYLYPQIGDRLDL 60

Qy   61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy  121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVCGSPRGGAVPRKP 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVCGSPRGGAVPRKP 180

Qy  181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy  241 GVAGAGAGAMCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GVAGAGAGAMCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy  301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
        ||||||||||||||||||||||  |||||||||||||||
Db  301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYY 338
```

RESULT 5
US-10-138-787-3
; Sequence 3, Application US/10138787
; Publication No. US20020172984A1
; GENERAL INFORMATION:
; APPLICANT: Holland, Sacha
; APPLICANT: Mbamalu, Geraldine
; APPLICANT: Pawson, Tony
; TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
; TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR

; TITLE OF INVENTION: TYROSINE KINASES
; FILE REFERENCE: 11757.23USWO
; CURRENT APPLICATION NUMBER: US/10/138,787
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/214,631
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/CA97/00473
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: 60/021,272
; PRIOR FILING DATE: 1996-07-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-138-787-3

  Query Match   75.0%; Score 1837; DB 4; Length 340;
  Best Local Similarity   99.7%; Pred. No. 1.3e-132;
  Matches 337; Conservative   1; Mismatches   0; Indels   0; Gaps   0;

```
Qy    1 MGPPHSGPGGVRVGALLLLGVLGVLSGLSLEPVYWNSANKRFQAEGGYVYLYPQIGDRLDL 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MGPPHSGPGGVRVGALLLLGVLGVLSGLSLEPVYWNSANKRFQAEGGYVYLYPQIGDRLDL 60

Qy   61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy  121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVCGSPRGGAVPRKP 180
        |||||||||||||||||||||||||||||||||||||||  |||||||||||||||||||
Db  121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVCQVGQSPRGGAVPRKP 180

Qy  181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy  241 GVAGAGAGAMCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GVAGAGAGAMCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy  301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
        ||||||||||||||||||||||  |||||||||||||||
Db  301 GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIYY 338
```

RESULT 6
US-10-417-924A-2
; Sequence 2, Application US/10417924A
; Publication No. US2003021591SA1
; GENERAL INFORMATION:
; APPLICANT: Samuel Davis, et al.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE EPH FAMILY LIGANDS
; FILE REFERENCE: REG-341Z
; CURRENT APPLICATION NUMBER: US/10/417,924A
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: 09/051,994
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: PCT/US96/17201
; PRIOR FILING DATE: 1996-10-25
; PRIOR APPLICATION NUMBER: 60/007,015
; PRIOR FILING DATE: 1995-10-25
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Misc. feature
; LOCATION: (166)
; OTHER INFORMATION: Xaa = unknown or other

US-10-417-924A-2

Query Match   74.9%;   Score 1835; DB 4; Length 340;
Best Local Similarity   99.7%; Pred. No. 1.8e-132;
Matches 337; Conservative   0; Mismatches   1; Indels   0; Gaps   0;

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Qy    1 MGPPHSGPGGVRVGALLLGLVSGLSLSLEPVYWNSANKRFQABGGYVLYPQIGDRLDL  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MGPPHSGPGGVRVGALLLGLVSGLSLSLEPVYWNSANKRFQABGGYVLYPQIGDRLDL  60

Qy   61 LCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy  121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
        |||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||
Db  121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLXVGQSPRGGAVPRKP 180

Qy  181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy  241 GVAGAGGANCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GVAGAGGANCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy  301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
        ||||||||||||||||||||||||||||||||||||||
Db  301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
```

RESULT 7
US-10-698-907-8

; Sequence 8, Application US/10698907
; Publication No. US20050049194A1
; GENERAL INFORMATION:
; APPLICANT: Frisen, Jonas
; APPLICANT: Holmberg, Johan
; TITLE OF INVENTION: Use of Ephrins and Related Molecules to Regulate Cellular
; TITLE OF INVENTION: Proliferation
; FILE REFERENCE: 21882-529 UTIL
; CURRENT APPLICATION NUMBER: US/10/698,907
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/460,488
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: US 10/291,290
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 60/393,272
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/345,206
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 8
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-698-907-8

Query Match   72.3%;   Score 1771; DB 5; Length 340;
Best Local Similarity   95.6%; Pred. No. 1.5e-127;
Matches 323; Conservative   7; Mismatches   8; Indels   0; Gaps   0;

```
Qy    1 MGPPHSGPGGVRVGALLLGLVSGLSLSLEPVYWNSANKRFQABGGYVLYPQIGDRLDL  60
        || ||:|||||| ||||||||:|||||||||||||||||||||||||||||||||||||
Db    1 MGPAHFGPGGQVGALLLGFAGLVSGLSLEPVYWNSANKRFQABGGYVLYPQIGDRLDL  60

Qy   61 LCPRARPPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
        |||||||||||||| :|.:|:|||||||||||||||||||||||||||||||||||||||
Db   61 LCPRARPPGPHSSPYEYLVEGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy  121 SPNLWGHEFRSHHDYYIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 SPNLWGHEFRSHHDYYIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
```

RESULT 8
US-10-408-765A-2695

; Sequence 2695, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumira S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2695
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-2695

Query Match   63.3%;   Score 1550; DB 4; Length 285;
Best Local Similarity   100.0%; Pred. No. 1.1e-110;
Matches 283; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

```
Qy   56 DRLDLLCPRARPGPHSSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTI 115
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 DRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTI  60

Qy  116 KFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGA 175
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 KFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGA 120

Qy  176 VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL 235
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL 180

Qy  236 ALLLLGVAGAGGANCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGI 295
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 ALLLLGVAGAGGANCWRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGI 240

Qy  296 ALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
        |||||||||||||||||||||||||||||||||||||||||||
Db  241 ALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 283
```

RESULT 9
US-10-698-907-7

; Sequence 7, Application US/10698907
; Publication No US20050049194A1
; GENERAL INFORMATION:
; APPLICANT: Frisen, Jonas
; APPLICANT: Holmberg, Johan
; TITLE OF INVENTION: Use of Ephrins and Related Molecules to Regulate Cellular

; ; ; ;

```
;   TITLE OF INVENTION: Proliferation
;   FILE REFERENCE: 21882-529 UTIL
;   CURRENT APPLICATION NUMBER: US/10/698,907
;   CURRENT FILING DATE:  2003-10-31
;   PRIOR APPLICATION NUMBER: US 60/460,488
;   PRIOR FILING DATE: 2003-04-03
;   PRIOR APPLICATION NUMBER: US 10/291,290
;   PRIOR FILING DATE: 2002-11-08
;   PRIOR APPLICATION NUMBER: US 60/393,272
;   PRIOR FILING DATE: 2002-07-02
;   PRIOR APPLICATION NUMBER: US 60/345,206
;   PRIOR FILING DATE: 2001-11-09
;   NUMBER OF SEQ ID NOS: 25
;   SOFTWARE: PatentIn version 3.2
;
;   SEQ ID NO 7
;   LENGTH: 336
;   TYPE: PRT
;   ORGANISM: Mus musculus
```

US-10-698-907-7

```
Query Match          25.7%;  Score 628.5;  DB 5;  Length 336;
Best Local Similarity 41.8%;  Pred. No. 7.3e-40;
Matches  137; Conservative  49; Mismatches 129; Indels  13; Gaps  5;
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```
Qy     14  GALLLLGVLGLVLSGLSLEPVYWNSANKRFQAEGGYVLLYPQIGDRLDLLCPRAPPGHSS  73
               |: ||:|                 |:|:|
Db     17  GLIMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLIYPQIGDKLDIICPKV---DSKTV  73

Qy     74  PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH  133
               |:|:|  |:|:|||||||||||||||||||||:|||||||| |:|
Db     74  GQYEYKYKVYMVKDKQADRCTIKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQXNK  133

Qy    134  DYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR  190
               ||:||            |:|:|||||||||||:|:
Db    134  DVYIISTNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSAARNHGPTRRPELEAGTN  193

Qy    191  GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVVAGAAGGLALLLLGVAGAGAMC  250
               |||||||||||||||||:||||||||||:|||||:|
Db    194  GRSSTTSPFVKENPGSSTDGNSAGHSGNNLLGSEVALPAGIASGCIIFIVIIITLVVLL  253

Qy    251  WRRRAKPSESRHPGPGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPH  310
               |||
Db    254  KYRRHRHKHSPQHTTTLSLTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH  306

Qy    311  YEKVSGDYGHPVIVQDGPPQSPPNIYY 338
               |:|||||||||||||:| |||| ||||
Db    307  YEKVSGDYGHPVIVQEMPPQSPANIYY 334
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```
RESULT 10
US-10-021-121-9
;   Sequence  9, Application US/10021121
;   Publication No. US20020142444A1
;   GENERAL INFORMATION:
;   APPLICANT: Caras, Ingrid W
;   TITLE OF INVENTION: A2-1 Neurotrophic Factor
;   NUMBER OF SEQUENCES: 10
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 1 DNA Way
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatin (Genentech)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/021,121
;   FILING DATE: 06-Dec-2001
;   CLASSIFICATION: <Unknown>
```

Second column:

```
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/635,130
;   FILING DATE: 19-Mar-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Torchia, PhD, Timothy E.
;   REGISTRATION NUMBER: 36,700
;   REFERENCE/DOCKET NUMBER: P1001
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650/225-8674
;   TELEFAX: 650/952-9981
;   INFORMATION FOR SEQ ID NO: 9:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 346 amino acids
;   TYPE: Amino Acid
;   TOPOLOGY: Linear
;
;   SEQUENCE DESCRIPTION: SEQ ID NO: 9:
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US-10-021-121-9

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Query Match          25.4%;  Score 623;  DB 4;  Length 346;
Best Local Similarity 39.2%;  Pred. No. 2e-39;
Matches  143; Conservative  48; Mismatches 116; Indels  58; Gaps  9;
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Qy      8  PGGVRVGALLLLGVLGLVSGL-------SLEPVYWNSANKRFQAEGGYVLLYPQIGDRLDLL  61
               ||: |:|  |||:|: |          :||||||||||||||||||||||||||||:|:|
Db      4  PGQRWLGKNLVAMVVWALCRIATPLAKNLEPVSWSSLNPKFLSCKGLVIYPKIGDKLDII  63

Qy     62  CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS  121
               ||||                  |:|:|||||||||||||||||||||||||||||||||
Db     64  CPRAEAGRP-----YEYYKYLVRPEQAAACSTVLDPNVLVTCNRPEQIRFTIKFQEFS  118

Qy    122  PNLWGHEFRSHHDYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQSPRGGAVPRKPV  181
               ||||| |:|:||  |:|:||||||||||||||||||||||||||:|:||:|:
Db    119  PNYMGLEFPKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT  178

Qy    182  SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVVAGAAGGLA---  236
               | ||  |:  | ||   |||||||||||||||||||||||||||||||||:||||
Db    179  SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-------GASGCGSSSGDPD  231

Qy    237  -----LLLLGVAGAGGA-----------MCWRRRAKPSESRHPGPGSFGRGGSLGL  277
                                                  ||||
Db    232  GFFNSKVALFAAVGAGCVIFLLIIFLTVLLLKLRKRHRKGHTQQ-------RAAALSL  282

Qy    278  ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVIVQDGPPQSP  333
                      |:|             |: :||| |||||||||||||||||||||||||:|
Db    283  STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVIVQEMPPQSP  339
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Qy    334  PNIYY 338
              |:|||
Db    340  ANIYY 344
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RESULT 11
US-10-356-289-2
;   Sequence  2, Application US/10356289
;   Publication No. US20040022767A1
;   GENERAL INFORMATION:
;   APPLICANT: Lyman, Stewart D.
;   APPLICANT: Beckmann, M. Patricia
;   APPLICANT: Baum, Peter R.
;   APPLICANT: Carpenter, Melissa K.
;   TITLE OF INVENTION: NOVEL CYTOKINE DESIGNATED ELK LIGAND
;   FILE REFERENCE: GENENT.67CPDV3
;   CURRENT APPLICATION NUMBER: US/10/356,289
;   CURRENT FILING DATE:  2003-01-31
;   PRIOR APPLICATION NUMBER: US/09/039,642B
;   PRIOR FILING DATE: 1998-03-16
;   PRIOR APPLICATION NUMBER: US/08/213,403
;   PRIOR FILING DATE: 1994-03-15
;   PRIOR APPLICATION NUMBER: 07/977,693
;   PRIOR FILING DATE: 1992-11-13
;   PRIOR APPLICATION NUMBER: 08/747,240
;   PRIOR FILING DATE: 1996-10-12
;   PRIOR APPLICATION NUMBER: 08/460,741
```

; ; ;

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; PRIOR FILING DATE: 1995-06-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;  TYPE: PRT
;  LENGTH: 346
; ORGANISM: Homo sapiens
US-10-356-289-2

Query Match    25.4%;  Score 623;  DB 4;  Length 346;
Best Local Similarity   39.2%;  Pred. No. 2e-39;
Matches 143;  Conservative  48;  Mismatches 116;  Indels  58;  Gaps  9;

Qy          8 PGGVRVGALLLLGVLGLVSGL-------SLEPVYWNSANKRFQAEGGYYLYLYPQIGDRLDLL 61
              ::|:::|||:||||||:|||        ::|||:||:||:||||::|:|||||:|||::||:
Db          4 PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy         62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
              |||::||||||:|||:||||||::|:::|||||:||||||||::||||||||::|:||
Db         64 CPRAEAGRP-----YEYXLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy        122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
              |||::|::|||||||:||:|::|::|:|:|||||||||||||||||:|:||||||||||
Db        119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy        182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
              |||::|:::|||:||  |||||||||||:|::||:||:||:|||||::|||||||
Db        179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-------GASGGSSGDPD 231

Qy        237 -------LLLLGVAGAGGA------------MCWRRRRAKPSESRHPGPGSFGRGGSLGL 277
                     |||||||||||             |||||:||||:||:|::|:||:||:||||
Db        232 GFFNSKVALFAAVGAGCVIFLLLIFLTVLLLKLRKRHRKHTQQ-------RAAALSL 282

Qy        278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                  ::|||||||:|||:||||:|:::|:||||:|||||||:||:|||||||:|:|||||
Db        283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVIVQEMPPQSP 339

Qy        334 PNIYY 338
              ||||
Db        340 ANIYY 344
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```
RESULT 12
US-10-712-124-60
; Sequence 60, Application US/10712124
; Publication No. US20040146907A1
; GENERAL INFORMATION:
;  APPLICANT: SMITH, VICTORIA
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING DYSPLASIA
;  FILE REFERENCE: P2000R1
;  CURRENT APPLICATION NUMBER: US/10/712,124
;  CURRENT FILING DATE: 2003-11-13
;  PRIOR APPLICATION NUMBER: US 60/425,813
;  PRIOR FILING DATE: 2002-11-13
;  NUMBER OF SEQ ID NOS: 123
;  SEQ ID NO 60
;   TYPE: PRT
;   LENGTH: 346
;  ORGANISM: Homo sapien
US-10-712-124-60

Query Match    25.4%;  Score 623;  DB 4;  Length 346;
Best Local Similarity   39.2%;  Pred. No. 2e-39;
Matches 143;  Conservative  48;  Mismatches 116;  Indels  58;  Gaps  9;

Qy          8 PGGVRVGALLLLGVLGLVSGL-------SLEPVYWNSANKRFQAEGGYYLYLYPQIGDRLDLL 61
              ::|:::|||:||||||:|||        ::|||:||:||:||||::|:|||||:|||::||:
Db          4 PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy         62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
              |||::||||||:|||:||||||::|:::|||||:||||||||::||||||||::|:||
Db         64 CPRAEAGRP-----YEYXLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy        122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
              |||::|::|||||||:||:|::|::|:|:|||||||||||||||||:|:||||||||||
Db        119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy        182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
              |||::|:::|||:||  |||||||||||:|::||:||:||:|||||::|||||||
Db        179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-------GASGGSSGDPD 231

Qy        237 -------LLLLGVAGAGGA------------MCWRRRRAKPSESRHPGPGSFGRGGSLGL 277
                     |||||||||||             |||||:||||:||:|::|:||:||:||||
Db        232 GFFNSKVALFAAVGAGCVIFLLLIFLTVLLLKLRKRHRKHTQQ-------RAAALSL 282

Qy        278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                  ::|||||||:|||:||||:|:::|:||||:|||||||:||:|||||||:|:|||||
Db        283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVIVQEMPPQSP 339

Qy        334 PNIYY 338
              ||||
Db        340 ANIYY 344
```

```
RESULT 13
US-10-789-378-30
; Sequence 30, Application US/10789378
; Publication No. US20050003390A1
; GENERAL INFORMATION:
;  APPLICANT: Axenovich, Sergey
;  APPLICANT: Stull, Robert
;  APPLICANT: Gelman, Marina
;  APPLICANT: Chui, Kitty
;  APPLICANT: Ng, Dean
;  TITLE OF INVENTION: DIAGNOSTIC METHODS FOR CANCER DETECTION
;  FILE REFERENCE: 5189-2
;  CURRENT APPLICATION NUMBER: US/10/789,378
;  CURRENT FILING DATE: 2004-02-26
;  PRIOR APPLICATION NUMBER: 10/441925
;  PRIOR FILING DATE: 2003-05-19
;  PRIOR APPLICATION NUMBER: 10/381619
;  PRIOR FILING DATE: 2002-05-17
;  PRIOR APPLICATION NUMBER: 60/450886
;  PRIOR FILING DATE: 2003-02-26
;  NUMBER OF SEQ ID NOS: 131
;  SOFTWARE: PatentIn version 3.1
;  SEQ ID NO 30
;   TYPE: PRT
;   LENGTH: 346
;  ORGANISM: Homo sapiens
US-10-789-378-30

Query Match    25.4%;  Score 623;  DB 5;  Length 346;
Best Local Similarity   39.2%;  Pred. No. 2e-39;
Matches 143;  Conservative  48;  Mismatches 116;  Indels  58;  Gaps  9;

Qy          8 PGGVRVGALLLLGVLGLVSGL-------SLEPVYWNSANKRFQAEGGYYLYLYPQIGDRLDLL 61
              ::|:::|||:||||||:|||        ::|||:||:||:||||::|:|||||:|||::||:
Db          4 PGQRWLGKWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy         62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
              |||::||||||:|||:||||||::|:::|||||:||||||||::||||||||::|:||
Db         64 CPRAEAGRP-----YEYXLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy        122 PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
              |||::|::|||||||:||:|::|::|:|:|||||||||||||||||:|:||||||||||
Db        119 PNYMGLEFKKHHDYYITSTSNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy        182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
              |||::|:::|||:||  |||||||||||:|::||:||:||:|||||::|||||||
Db        179 SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-------GASGGSSGDPD 231

Qy        237 -------LLLLGVAGAGGA------------MCWRRRRAKPSESRHPGPGSFGRGGSLGL 277
                     |||||||||||             |||||:||||:||:|::|:||:||:||||
Db        232 GFFNSKVALFAAVGAGCVIFLLLIFLTVLLLKLRKRHRKHTQQ-------RAAALSL 282

Qy        278 ----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
                  ::|||||||:|||:||||:|:::|:||||:|||||||:||:|||||||:|:|||||
Db        283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVIVQEMPPQSP 339

Qy        334 PNIYY 338
              ||||
Db        340 ANIYY 344
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Qy  278  -----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP  333
              ||||||||||||||||||||:||:|||||||:|||||
Db  283  STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP  339

Qy  334  PNIYY  338
         |||||
Db  340  ANIYY  344


RESULT 14
US-10-698-907-14

; Sequence 14, Application US/10698907
; Publication No. US20050049194A1
; GENERAL INFORMATION:
;   APPLICANT: Frisen, Jonas
;   APPLICANT: Holmberg, Johan
;   TITLE OF INVENTION: Use of Ephrins and Related Molecules to Regulate Cellular
;      TITLE OF INVENTION: Proliferation
;   FILE REFERENCE: 21882-529 UTIL
;   CURRENT APPLICATION NUMBER: US/10/698,907
;   CURRENT FILING DATE: 2003-10-31
;   PRIOR APPLICATION NUMBER: US 60/460,488
;   PRIOR FILING DATE: 2003-04-03
;   PRIOR APPLICATION NUMBER: US 10/291,290
;   PRIOR FILING DATE: 2002-11-08
;   PRIOR APPLICATION NUMBER: US 60/393,272
;   PRIOR FILING DATE: 2002-07-02
;   PRIOR APPLICATION NUMBER: US 60/345,206
;   PRIOR FILING DATE: 2001-11-09
;   NUMBER OF SEQ ID NOS: 25
;   SOFTWARE: Patentin version 3.2
;
; SEQ ID NO 14
;   LENGTH: 346
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-698-907-14

  Query Match      25.4%;  Score 623;  DB 5;  Length 346;
  Best Local Similarity   39.2%;  Pred. No. 2e-39;
  Matches  143;  Conservative  48;  Mismatches 116;  Indels 58;  Gaps  9;

Qy    8  PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLFVPQIGDRLDLL   61
             |:||  |:|:|  :| :|:||
Db    4  PGORWLGKWLVAMVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII   63

Qy   62  CPRARPPGPHSSPSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS  121
            |:||:||   :||||  ||||:||
Db   64  CPRAEAGRP------YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS  118

Qy  122  PNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV  181
            :||||||||||||||||||||||:||
Db  119  PNYMGLEFKKHHDYYITSTNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT  178

Qy  182  SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA----  236
            :||| ::|
Db  179  SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVNQEEKSGP-----GASGGSSGDPD  231

Qy  237  --------LLLLGVAGAGGA------------MCWRRRRAKPSESRHPGPGSFGRGGSLGL  277
Db  232  GFFNSKVALFAAVGAGCVIFLLIIFLTVLLLKLRKRHRKHTQQ--------RAAALSL  282

Qy  278  -----GGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP  333
Db  283  STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP  339

Qy  334  PNIYY  338
Db  340  ANIYY  344
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;  Patent No. US2001009768A1
;  GENERAL INFORMATION:
;   APPLICANT: Cerretti, Douglas
;   APPLICANT: Reddy, Pranhitha
;   TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING CYTOKINE DESIGNATED LERK-5
;   FILE REFERENCE: 28232
;   CURRENT APPLICATION NUMBER: US/09/754,105
;   CURRENT FILING DATE: 2001-01-03
;   PRIOR APPLICATION NUMBER: 09/329,531
;   PRIOR FILING DATE: 1999-06-10
;   NUMBER OF SEQ ID NOS: 3
;   SOFTWARE: Patentin version 3.0
;
; SEQ ID NO 2
;   LENGTH: 333
;   TYPE: PRT
;   ORGANISM: homo sapiens
US-09-754-105-2

  Query Match      25.3%;  Score 620.5;  DB 3;  Length 333;
  Best Local Similarity   40.5%;  Pred. No. 3e-39;
  Matches  133;  Conservative  52;  Mismatches 130;  Indels 13;  Gaps  5;

Qy   14  GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLFVPQIGDRLDLCPRARPPGHSS   73
            |:|  ||||||||||:|||||
Db   14  GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV   70

Qy   74  PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH  133
            |:||:||  |||||||||  |||:||||:|||||||||:||||||||||:||  |:|
Db   71  GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQRNK  130

Qy  134  DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVVSEMPMER-DR  190
            ||||:|| :|:|||:|: ||||  :|| ||::|||
Db  131  DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQODASSAGSTRNKDPTRRPELEAGTN  190

Qy  191  GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC  250
            :   ||                                    :|: :| :
Db  191  GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIILLVVLLL  250

Qy  251  WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH  310
            |||  :  |                                       |||||:|||
Db  251  KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN---NGSEPSDIIIPLR---TADSVFCPH  303

Qy  311  YEKVSGDYGHPVYIVQDGPPQSPNIYY  338
            |||||||||||||||:|:|||||:|||
Db  304  YEKVSGDYGHPVYIVQEMPPQSPANIYY  331
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Search completed: December 21, 2005, 14:41:50
Job time : 130.201 secs

RESULT 15
US-09-754-105-2
; Sequence 2, Application US/09754105

OM protein - protein search, using sw model

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

Run on: December 21, 2005, 14:21:53 ; Search time 176.277 Seconds
(without alignments)
1821.088 Million cell updates/sec

Title: US-10-021-121-2
Perfect score: 2450
Sequence: 1 MGPPHSGPGGVRGALILLG..........TTLLRQRASVEAEAGQHGPL 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 70552306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1841	75.1	340	1	EFNB3_HUMAN	Q15768 homo sapien
2	1771	72.3	340	1	EFNB3_MOUSE	O35393 mus musculu
3	1771	72.3	340	1	EFNB3_MOUSE	Q5F221 mus musculu
4	914	37.3	331	2	Q90231_BRARE	Q90231 brachydanio
5	914	37.3	342	2	Q502Q3_BRARE	Q502Q3 brachydanio
6	910	37.1	327	2	Q9PT69_XENLA	Q9PT69 xenopus lae
7	628.5	25.7	336	1	EFNB2_MOUSE	P52800 mus musculu
8	628.5	25.7	336	1	EFNB2_MOUSE	P52800 mus musculu
9	628.5	25.4	336	2	Q4FJM3_MOUSE	Q4FJM3 mus musculu
10	623	25.3	346	1	EFNB1_HUMAN	P98172 homo sapien
11	620.5	25.3	333	1	EFNB1_HUMAN	P98172 homo sapien
12	620.5	25.3	333	2	Q5JV56_HUMAN	Q5JV56 homo sapien
13	620.5	25.3	333	2	Q9PU04_CHICK	Q9PU04 gallus gall
14	619	25.3	334	1	EFNB1_CHICK	P52799 gallus gall
15	617.5	25.2	332	1	EFNB2_BRARE	Q90Z33 brachydanio
16	607	24.8	341	2	Q90Z33_BRARE	Q90Z33 brachydanio
17	606.5	24.8	345	2	Q6P7B6_RAT	Q6P7B6 rattus norv
18	604.5	24.7	345	2	Q6P7B6_RAT	Q6P7B6 rattus norv
19	604.5	24.5	345	1	EFNB1_MOUSE	P52795 mus musculu
20	604.5	24.5	345	1	EFNB1_MOUSE	P52795 mus musculu
21	599.5	24.3	329	2	Q54419_MOUSE	Q54419 mus musculu
22	596.5	24.3	334	2	Q6PF53_XENLA	Q6PF53 xenopus lae
23	596.5	24.1	327	2	Q90Z32_BRARE	Q90Z32 brachydanio
24	591	22.8	324	2	EFNB1_XENLA	O13097 xenopus lae
25	559.5	18.1	204	2	Q4SH26_TETNG	Q4SH26 tetraodon n
26	443	16.4	386	2	Q4T7D5_TETNG	Q4T7D5 tetraodon n
27	401	14.3	359	2	Q4RK83_TETNG	Q4RK83 tetraodon n
28	349.5	13.9	217	2	Q4H18_CIOIN	Q4H18 ciona intes
29	341.5	13.5	205	2	Q5JV57_HUMAN	Q5JV57 homo sapien
30	341.5	10.3	97	2	Q9WH9_XENLA	Q9W6H9 xenopus lae
31	331	13.5	205	2	Q9W6H9_XENLA	Q9W6H9 xenopus lae
32	205	8.4	182	2	Q4RT95_TETNG	Q4RT95 tetraodon n
33	198.5	8.1	279	2	Q9U474_CAEEL	Q9U474 caenorhabdi
34	198	8.1	278	2	Q61HF9_CAEBR	Q61HF9 caenorhabdi
35	192	7.8	652	2	Q9V4E1_DROME	Q9V4E1 drosophila
36	185	7.6	195	1	EFNA2_BRARE	P79727 brachydanio
37	184.5	7.5	428	2	Q5TXC6_ANOGA	Q5txc6 anopheles g
38	182	7.4	260	2	Q6VU49_MANSE	Q6vu49 manduca sex
39	179	7.3	238	1	EFNA3_HUMAN	P52797 homo sapien
40	178.5	7.3	202	2	Q98TZ1_CHICK	Q98tz1 gallus gall
41	176	7.2	209	1	EFNA2_MOUSE	P52801 mus musculu
42	175.5	7.2	213	1	EFNA2_HUMAN	O43921 homo sapien
43	172.5	7.0	217	2	Q5M7P3_XENTR	Q5m7p3 xenopus tro
44	172	7.0	200	1	EFNA2_CHICK	P52802 gallus gall
45	170.5	7.0	228	1	EFNA5_CHICK	P52804 gallus gall

ALIGNMENTS

RESULT 1
EFNB3_HUMAN
ID   EFNB3_HUMAN   STANDARD;   PRT;   340 AA.
AC   Q15768; O00680; Q87BH7; Q92875;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ephrin-B3 precursor (EPH-related receptor tyrosine kinase ligand 8)
DE   (LERK-8) (EPH-related receptor transmembrane ligand ELK-L3).
GN   Name=EFNB3; Synonyms=EPLG8, LERK8;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=97271551; PubMed=9126477; DOI=10.1006/geno.1997.4615;
RA   Tang X.X., Pleasure D.E., Ikegaki N.;
RT   "cDNA cloning, chromosomal localization, and expression pattern of
RT   EPLG8, a new member of the EPLG gene family encoding ligands of EPH-
RT   related protein-tyrosine kinase receptors.";
RL   Genomics 41:17-24(1997).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RA   Cerretti D.P.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain cortex;
RX   MEDLINE=96404527; PubMed=8808709;
RA   Gale N.W., Flenniken A., Compton D.C., Jenkins N.A., Copeland N.G.,
RA   Gilbert D.J., Davis S., Wilkinson D.G., Yancopoulos G.D.;
RT   "Elk-L3, a novel transmembrane ligand for the Eph family of receptor
RT   tyrosine kinases, expressed in embryonic floor plate, roof plate and
RT   hindbrain segments.";
RL   Oncogene 13:1343-1352(1996).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Brain;
RX   MEDLINE=22382257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

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RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   PROTEIN SEQUENCE OF 28-42.
RA   Zhang Z., Henzel W.J.;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
RN   [6]
RP   INTERACTIONS WITH GRIP1 AND GRIP2.
RC   TISSUE=Fetal brain;
RX   MEDLINE=99211388; PubMed=10197531; DOI=10.1016/s0896-6273(00)80706-0;
RA   Brueckner K., Pablo Labrador J., Scheffele P., Herb A., Seeburg P.H.,
RA   Klein R.;
RT   "EphrinB ligands recruit GRIP family PDZ adaptor proteins into raft
RT   membrane microdomains.";
RL   Neuron 22:511-524(1999).
CC   -!- FUNCTION: May play a pivotal role in forebrain function. Binds to,
CC       and induce the collapse of, commissural axons/growth cones in
CC       vitro. May play a role in constraining the orientation of
CC       longitudinally projecting axons (By similarity).
CC   -!- SUBUNIT: Interacts with GRIP1 and GRIP2.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Highly expressed in brain; expressed in
CC       embryonic floor plate, roof plate and hindbrain segments.
CC   -!- SIMILARITY: Belongs to the ephrin family.
```

```
DR   EMBL; U57001; AAB05170.1; -; mRNA.
DR   EMBL; U66406; AAC51203.1; -; mRNA.
DR   EMBL; U62775; AAC50707.1; -; mRNA.
DR   EMBL; BC022499; AAH22499.1; -; mRNA.
DR   EMBL; BC042944; AAH42944.1; -; mRNA.
DR   HSSP; P52800; 1IKO.
DR   Ensembl; ENSG00000108947; Homo sapiens.
DR   HGNC; HGNC:3228; EFNB3.
DR   MIM; 602297; -.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; Ephrin.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005005; F:transmembrane-ephrin receptor activity; TAS.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0007399; P:neurogenesis; TAS.
KW   Developmental protein; Differentiation; Direct protein sequencing;
KW   Glycoprotein; Neurogenesis; Polymorphism; Signal; Transmembrane.
FT   SIGNAL        1     27
FT   CHAIN        28    340       Ephrin-B3.
FT   TOPO_DOM     28    226       Extracellular (Potential).
FT   TRANSMEM    227    247       Potential.
FT   TOPO_DOM    248    340       Cytoplasmic (Potential).
FT   MOTIF       338    340       PDZ recognition motif (Potential).
FT   CARBOHYD    210    210       N-linked (GlcNAc...) (Potential).
FT   DISULFID     62    104       By similarity.
FT   DISULFID     92    156       By similarity.
FT   VARIANT     166    166       R -> Q.
FT                               /FTId=VAR_002356.
SQ   SEQUENCE   340 AA;  35835 MW;  EDFP2A23C2FDE79F CRC64;
```

```
Query Match             75.1%;  Score 1841;  DB 1;  Length 340;
  Best Local Similarity   100.0%;  Pred. No. 1e-110;
  Matches  338;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVTWNSANKRFQAEGGYVLYPIGDRLDL 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVTWNSANKRFQAEGGYVLYPIGDRLDL 60

Qy   61 LCPRARPGGPHSSPNYEYKLYLYPGGAQGRRCEAPPANLLLTCDRPDLDLRFIKFQEY 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 LCPRARPGGPHSSPNYEYKLYLYPGGAQGRRCEAPPANLLLTCDRPDLDLRFIKFQEY 120

Qy  121 SPNLWGHEFRSHHDYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 SPNLWGHEFRSHHDYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy  181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGLALLL 240
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGLALLL 240

Qy  241 GVAGAGGAMCWRRRRAKPSESRHPGPGSPGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  241 GVAGAGGAMCWRRRRAKPSESRHPGPGSPGRGGSLGLGGGGGMGPREAEPGELGIALRGG 300

Qy  301 GAADPPFCPHYEKVSGDYGHPVIVQDGPPQSPPNIIY 338
         |||||||||||||||||||||||||||||||||||||
Db  301 GAADPPFCPHYEKVSGDYGHPVIVQDGPPQSPPNIIY 338

RESULT 2
EFNB3_MOUSE

ID   EFNB3_MOUSE             STANDARD;      PRT;   340 AA.
AC   O35393;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ephrin-B3 precursor.
GN   Name=Efnb3;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=98143367; PubMed=9484836; DOI=10.1038/sj.onc.1201557;
RA   Bergemann A.D., Zhang L., Chiang M.-K., Brambilla R., Klein R.,
RA   Flanagan J.G.;
RT   "Ephrin-B3, a ligand for the receptor EphB3, expressed at the midline
RT   of the developing neural tube.";
RL   Oncogene 16:471-480(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
```

RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN   [3]
RP   FUNCTION.
RX   MEDLINE=20171264; PubMed=10704386;
RA   Imondi R., Wideman C., Kaprielian Z.;
RT   "Complementary expression of transmembrane ephrins and their receptors
RT   in the mouse spinal cord: a possible role in constraining the
RT   orientation of longitudinally projecting axons.";
RL   Development 127:1397-1410(2000).
CC   -!- FUNCTION: May play a pivotal role in forebrain function. Binds to,
CC   and induce the collapse of, commissural axons/growth cones in
CC   vitro. May play a role in constraining the orientation of
CC   longitudinally projecting axons.
CC   -!- SUBUNIT: Interacts with GRIP1 and GRIP2 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed on lateral floor plate cells,
CC   specifically on commissural axon segments that have passed through
CC   the floor plate. Expressed in cells of the retinal ganglion cell
CC   layer during retinal axon guidance to the optic disk.
CC   -!- DEVELOPMENTAL STAGE: Expressed in the floor plate throughout the
CC   period of commissural axon pathfinding.
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   EMBL; AF025288; AAC53537.1; -; mRNA.
DR   EMBL; BC052001; AAH52001.1; -; mRNA.
DR   EMBL; BC056617; AAH56617.1; -; mRNA.
DR   Ensembl; ENSMUSG00000003934; Mus musculus.
DR   HSSP; P52800; 1IKO.
DR   MGI; MGI:109196; Efnb3.
DR   GO; GO:0005615; C:extracellular space; TAS.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   GO; GO:0007628; P:adult walking behavior; IMP.
DR   GO; GO:0016198; P:axon choice point recognition; IMP.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Differentiation; Glycoprotein; Neurogenesis;
KW   Signal; Transmembrane.
FT   SIGNAL   1   27   Potential.
FT   CHAIN   28   340   Ephrin-B3.
FT   TOPO_DOM   28   227   Extracellular (Potential).
FT   TRANSMEM   228   248   Potential.
FT   TOPO_DOM   249   340   Cytoplasmic (Potential).
FT   MOTIF   338   340   PDZ recognition motif (Potential).
FT   CARBOHYD   210   210   N-linked (GlcNAc...) (Potential).
FT   DISULFID   62   104   By similarity.
FT   DISULFID   92   156   By similarity.
SQ   SEQUENCE   340 AA; 35885 MW; 52F3D58FD209A6B8 CRC64;

Query Match   72.3%; Score 1771; DB 1; Length 340;
Best Local Similarity   95.6%; Pred. No. 3.4e-106;
Matches 323 Conservative   7; Mismatches   8; Indels   0; Gaps   0;

Qy   1 MGPPHSGPGGVRVGALLILLGVGLSVSGLSLEPVYWNSANKRFQAEGGTVYLYPQIGDRLDL 60
              || ||||| |||| |||||||||:| ||||||||||||||||||||||||||||||||||||
Db   1 MGAPHFGPGGVQVGALLLLGFAGLVSGLSLEPVYWNSANKRFQABGGTVYLYPQIGDRLDL 60

Qy   61 LCPRARPPGPHSSPNYEYKYLVGGAGQRRCEAPPAPNLLTCDRPDLDLRFTIKFQEY 120
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db   61 LCPRARPPGPHSSPYEFKYLVLVBGAGQRRCEAPPAPNLLTCDRPDLDLRFTIKFQEY 120

Qy   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

RESULT 3

Q5F221_MOUSE

ID   Q5F221_MOUSE PRELIMINARY;   PRT;   340 AA.
AC   Q5F221;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Ephrin B3 (16 days embryo head cDNA, RIKEN full-length enriched
DE   library, clone:C130048B01 product:m-ephrin-B3).
GN   Name=Efnb3; ORFNames=RP23-56I20.5-001;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Tromans A.;
RL   Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bareh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,

Qy   181 VSEMPMERDRGAAHSLEPGKENLPCDPTSNATSRGAEGPLPPPSMPAVAGGILALLLL 240
              ||||||||||||| ||:: |||||||||||||||||||||||||||||||||||||||
Db   181 VSEMPMERDRGAAHSAEPGRDTIPGDPSSNATSRGAEGPLPPPSMPAVAGAAGGMALLLL 240

Qy   241 GVAGAGGAMCWRRRAKPSESSRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG 300
              ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GVAGAGGAMCWRRRAKPSESSRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG 300

Qy   301 GAADPPFCHYEKVSGDYGHPVYIVQDGPPSQSPPNIYY 338
              |||||||||||||||||||||||||||||||||||||
Db   301 GTADPPFCHYEKVSGDYGHPVYIVQDGPPSQSPPNIYY 338

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RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawagawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wiming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=C57BL/6J; TISSUE=Head;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
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Db   121  SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP  180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121  SPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKP  180

Qy   181  VSEMPMERDRGAAHSLEPGKENLPGDPPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL  240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181  VSEMPMERDRGAAHSAEPGRDTIPGDPSSNATSRGAEGPLPPPSMPAVAGAAGMALLLL   240

Qy   241  GVAGAGGAMCWRRRRAKPSESRIHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG  300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241  GVAGAGGAMCWRRRRAKPSESRIHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGG  300

Qy   301  GAADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIY  338
          ||||||||||||||||||||||||||||||||||||||
Db   301  GTADPPFCPHYEKVSGDYGHPVVIVQDGPPQSPPNIY  338
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RESULT 4

```
Q90231_BRARE

AC   Q90231;
ID   Q90231_BRARE   PRELIMINARY;   PRT;   331 AA.
AC   Q90231;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ephrin B3.
GN   Name=efnb3;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21290827; PubMed=11397014; DOI=10.1006/dbio.2001.0281;
RA   Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
RA   Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;
RT   "Morphogenesis of prechordal plate and notochord requires intact
RT   eph/ephrin b signaling.";
RL   Dev. Biol. 234:470-482(2001).
DR   EMBL; AF375227; AAK64277.1; -; mRNA.
DR   HSSP; P52800; 11KO.
DR   Ensembl; ENSDARG00000008177; Danio rerio.
DR   ZFIN; ZDB-GENE-010618-3; efnb3.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; Ephrin; 1.
SQ   SEQUENCE   331 AA;   35638 MW;   6A5EACD5O9AO9818 CRC64;
```

Bottom alignment (left):

```
Qy   Query Match
     Best Local Similarity 95.6%;
     Matches 323; Conservative 7;     Mismatches 8; Indels 0; Gaps 0;
     Score 1771; DB 2; Length 340;    Pred. No. 3.4e-106;

1    MGPPHSGPCGVRVGALLLGVLGVLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL  60
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Bottom alignment (right):

```
Qy   Query Match
     Best Local Similarity 54.5%;
     Matches 188; Conservative 43;    Mismatches 74; Indels 40; Gaps 10;
     Score 914; DB 2; Length 331;     Pred. No. 5.4e-51;

Qy   10   GVRVGALLLGVLGVLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPG   69
          || :|  ||  | ||||  |:|  |:|||| |||| .: ||||||||||||| |  ||
Db   10   GLGILIFLVDLLG-ITATNMEPIYWNSLNKRFSDDKGVVLYPQIGDRLDLICPSSDPPG   67

Qy   70   PHSSPNYEYKLYLVGG-AQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHE   127
          || ||:| : ||:|:|| | |  | :|| || :|||| ::| |: ||:|| |||:|| ||
Db   68   PRAPADYEYKLYLVSSREQADRCEVTGAPNLLLTCDKPNSDMRFTIKFQEYSPNLWGHE   128

Qy   129  FRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRG-GAVPRKPVSEMPME   187
          |:||||||:||||||||:||||| |||| ||||:||:|| ||| | |||  ||| |:   :
Db   128  FKTNHDYFIIATSDGTRQGLESMRGGVCATQGMKVLKVGQSPYGLPAKSPKPDS-----  182
```

RESULT 5

```
Qy  188 RDRGAAHSLEPGKENLPGDPTSNAT----------SRGAEGPLPPPSMPAVAGAACGLALLL 239
            |:|:|              |:|      ::  ||||||||| ||
Db  183 ----------AGRINNPNPGTGNSTHPQIPPRGSGGENGPLPASNIAVIAGAAGGSAFLL 232

Qy  240 LGVAGAGGAMCWRRRARAKPSESRHPGPGSFG------RGGSLGLGGGGMGPREAEPGEL 293
            |||||||| ||  : |: ::|| ::|||| :  ::  ||||| | |||| ||| ||||
Db  233 L-VTAVICVVCYRRRHAKHSESHHP-PLSLSLTSPKRCGCGVGGGNNNG---SEPSDI 287

Qy  294 GIALRGGGAADPPPCPHYEKVSGDYGHPVYIVQDGPPQSPPNIIY 338
            ||||||||||   | ||||||||||||||||||::  |||:|||
Db  288 IIPLR---TSDSAYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYY 329
```

ID   Q50ZQ3_BRARE PRELIMINARY;   PRT;   342 AA.
AC   Q50ZQ3;
DT   13-SEP-2005 (TrEMBLrel. 31, Created)
DT   13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Efnb3 protein.
GN   Name=efnb3;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McKernan P.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RG   NIH MGC Project;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC095605; AAH95605.1; -; mRNA.
SQ   SEQUENCE 342 AA; 36885 MW; 1629532234F85386 CRC64;

Query Match   37.3%; Score 914; DB 2; Length 342;
Best Local Similarity   54.5%;
Matches 188; Conservative 43; Mismatches 74; Indels 40; Gaps 10;

```
Qy   10 GVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPG 69
Db   20 GLGTLLIFLVDLLG-ITATNMEPIYWNSLNKRFSDDKGYVLYPQIGDRLDLICPSSDPPG 78

Qy   70 PHSSPNYEFYKLYLVGG-AQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHE 128
Db   79 PRAPADVEYYKLYLVSSREQADRCEVTGAPNLLLTCDKPNSDMRFTIKFQEYSPNLWGHE 138

Qy  129 FRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRG-GAVPRKEVSEMPME 187
Db  139 FRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKEVSEMPME 187
```

RESULT 6

```
Db  139 FKTNHDYFIIATSDGTDRQGLESMRGGVCATQGMKVVLKVGQSPYGLPAKSPKPDS----- 193
            |:| ||| |||||||  ||||:|||||| :||||:||:||||| ||   ||   :
Qy  188 RDRGAAHSLEPGKENLPGDPTSNAT----------SRGAEGPLPPPSMPAVAGAACGLALLL 239

Db  194 ------AGRINNPNPGTGNSTHPQIPPRGSGGENGPLPASNIAVIAGAAGGSAFLL 243
Qy  240 LGVAGAGGAMCWRRRARAKPSESRHPGPGSFG------RGGSLGLGGGGMGPREAEPGEL 293
Db  240 L-VTAVICVVCYRRRHAKHSESHHP-PLSLSLTSPKRCGCGVGGGNNNG---SEPSDI 298

Qy  294 GIALRGGGAADPPPCPHYEKVSGDYGHPVYIVQDGPPQSPPNIIY 338
            ||||||||||   | ||||||||||||||||||::  |||:|||
Db  299 IIPLR---TSDSAYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYY 340
```

ID   Q9PT69_XENLA PRELIMINARY;   PRT;   327 AA.
AC   Q9PT69;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Ephrin-B3 precursor.
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Embryonic head;
RX   MEDLINE=20099673; PubMed=10633856;
RA   Helbling P.M., Saulnier D.M.E., Robinson V., Christiansen J.H.,
RA   Wilkinson D.G., Brandli A.W.;
RT   "Comparative analysis of embryonic gene expression defines potential
RT   interaction sites for Xenopus EphB4 receptors with ephrin-B ligands.";
RL   Dev. Dyn. 216:361-373(1999).
RN   [2]
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ236866; CAB65511.1; -; mRNA.
DR   HSSP; P52800; 1IKO.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR002086; Aldehyd_dehydrog.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   PRODom; PD005533; Ephrin; 1.
DR   PROSITE; PS006887; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Signal.
FT   SIGNAL   1   25   Potential.
SQ   SEQUENCE 327 AA; 35913 MW; 4BB0FA39D4C22DCD CRC64;

Query Match   37.1%; Score 910; DB 2; Length 327;
Best Local Similarity   60.1%; Pred. No. 9.7e-51;
Matches 190; Conservative 30; Mismatches 82; Indels 14; Gaps 8;

```
Qy   25 VSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPGPHSSPNYEFYKLYLV 84
Db   22 ISALSLDPIYWNSSNKRFEDTEGYVLYPQIGDRLDLLCPRSEPQGFPSSSSPYEYKLYLV 81

Qy   85 GGAQG-RRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDG 143
Db   82 GTKEEMSSCCILRTPNLLLTCDRPSQDLRFTIKFQEFSPNLWGHEFQSQDYYIIATSDG 141

Qy  144 TREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPERDRGAAHSL-EPGKEN 202
Db  142 TMDGIETLQGGVCETKGMKVTLKVGQSPNGATPPRRPSS---AGKDSGISPSVPNDIPN 198

Qy  203 LPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESR 262
Db  199 V-GFSGNATKTGENGPLPISHVPLVAGAGGAALLLL-VFGVGVGWVCHRRRQQAKHSDTR 256

Qy  263 HPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGGGAADPPPCPHYEKVSGDYGHPV 322
Db  257 ............................................ 322
```

```
Db    ||      ||  ||||  |   ||||   ||  |||||||||||||||||||||
      HP-PLSLGSITSPKRGNN----NGHEPSDIIMPLRPSEAG--AFCPHYEKVSGDYGHPV
Qy    257                                                        309
      ||| ||  |||| ||||  |  |  |||||   |||  |||||  ||||  |
Qy    323 YIVQDGPPQSPPNIYY                                        338
         ||||| ||||||| ||||
Db    310 YIVQDMASQSPANIYY                                        325
```

RESULT 7
EFNB2_MOUSE

ID   EFNB2_MOUSE   STANDARD;   PRT;   336 AA.
AC   P52800;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ephrin-B2 precursor (EPH-related receptor tyrosine kinase ligand 5)
DE   (LERK-5) (HTK ligand) (HTK-L) (ELF-2).
GN   Name=Efnb2; Synonyms=Elf2, Epl5, Eplg5, Htkl, Lerk5;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=96145233; PubMed=8559144; DOI=10.1016/0161-5890(95)00108-5;
RA   Cerretti D.P., Vanden Bos T., Nelson N., Kozlosky C.J., Reddy P.,
RA   Maraskovsky E., Park L.S., Lyman S.D., Copeland N.G., Gilbert D.J.,
RA   Jenkins N.A., Fletcher R.A.;
RT   "Isolation of LERK-5: a ligand of the eph-related receptor tyrosine
RT   kinases.";
RL   Mol. Immunol. 32:1197-1205(1995).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=95199254; PubMed=7534404;
RA   Bennett B.D., Zeigler F.C., Gu Q., Fendly B., Goddard A.D.,
RA   Gillett N., Matthews W.;
RT   "Molecular cloning of a ligand for the EPH-related receptor protein-
RT   tyrosine kinase Htk.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:1866-1870(1995).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=ICR; TISSUE=Brain;
RX   MEDLINE=95379837; PubMed=7651410;
RA   Bergemann A.D., Cheng H.J., Brambilla R., Klein R., Flanagan J.G.;
RT   "ELF-2, a new member of the Eph ligand family, is segmentally
RT   expressed in mouse embryos in the region of the hindbrain and newly
RT   forming somites.";
RL   Mol. Cell. Biol. 15:4921-4929(1995).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan R., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McKernan P.J., McEwan K.J., Malek J.A., Gay L.J., Hulyk S.W.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   FUNCTION.
RX   MEDLINE=20171264; PubMed=10704386;
RA   Imondi R., Wideman C., Kaprielian Z.;
RT   "Complementary expression of transmembrane ephrins and their receptors
RT   in the mouse spinal cord: a possible role in constraining the
RT   orientation of longitudinally projecting axons.";
RL   Development 127:1397-1410(2000).
RN   [6]
RP   X-RAY CRYSTALLOGRAPHY (1.92 ANGSTROMS) OF 30-170.
RX   PubMed=11739926; DOI=10.1016/S1534-5807(01)00002-8;
RA   Toth J., Cutforth T., Gelinas A.D., Bethoney K.A., Bard J.,
RA   Harrison C.J.;
RT   "Crystal structure of an ephrin ectodomain.";
RL   Dev. Cell 1:83-92(2001).
RN   [7]
RP   X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 31-168 IN COMPLEX WITH EPHB2.
RX   PubMed=11780699; DOI=10.1038/414933a;
RA   Himanen J.-P., Rajashankar K.R., Lackmann M., Cowan C.A.,
RA   Henkemeyer M., Nikolov D.B.;
RT   "Crystal structure of an Eph receptor-ephrin complex.";
RL   Nature 414:933-938(2001).
CC   -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB2 and EPHB4.
CC   May play a role in constraining the orientation of longitudinally
CC   projecting axons.
CC   -!- SUBUNIT: Interacts with PDZRN3 (By similarity). Binds to the
CC   receptor tyrosine kinase EPHB4.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed on lateral floor plate cells,
CC   specifically on commisural axon segments that have passed through
CC   the floor plate. Expressed in cells of the retinal ganglion cell
CC   layer during retinal axon guidance to the optic disk.
CC   -!- DEVELOPMENTAL STAGE: Expressed in the floor plate throughout the
CC   period of commissural axon pathfinding.
CC   -!- PTM: Inducible phosphorylation of tyrosine residues in the
CC   cytoplasmic domain (By similarity).
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC   --
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --
DR   EMBL; U16819; AAA99708.1; -; mRNA.
DR   EMBL; L38847; AAC42052.1; -; mRNA.
DR   EMBL; U30244; AAB29314.1; -; mRNA.
DR   EMBL; BC057009; AAH57009.1; -; mRNA.
PIR; I49766; I49766.
PDB; 1IKO; X-ray; P=30-207.
PDB; 1KGY; X-ray; E/F/G/H=31-168.
Ensembl; ENSMUSG00000001300; Mus musculus.
MGI; MGI:105097; Efnb2.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0005886; C:plasma membrane; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0001945; P:lymph vessel development; IMP.
GO; GO:0009887; P:organogenesis; IMP.
InterPro; IPR001799; Ephrin.
Pfam; PF00812; Ephrin; 1.
PRINTS; PR01347; EPHRIN.
ProDom; PD002533; Ephrin; 1.
PROSITE; PS01299; EPHRIN; 1.
KW   3D-structure; Developmental protein; Differentiation; Glycoprotein;
KW   Neurogenesis; Phosphorylation; Signal; Transmembrane.
FT   SIGNAL   1   28
FT   CHAIN   29   336   Ephrin-B2.
FT   TOPO_DOM   29   232   Extracellular (Potential).
FT   TRANSMEM   233   253   Potential.
FT   TOPO_DOM   254   336   Cytoplasmic (Potential).
FT   MOTIF   334   336   PDZ recognition motif (Potential).
```

```
FT   CARBOHYD      39     39       N-linked (GlcNAc...).
FT   CARBOHYD     142    142       N-linked (GlcNAc...) (Potential).
FT   DISULFID      65    104
FT   DISULFID      92    156
FT   CONFLICT       3      4       Missing (in Ref. 3).
FT   CONFLICT     177    177       A -> T (in Ref. 1).
FT   STRAND        36     37
FT   TURN          40     41
FT   STRAND        43     44
FT   TURN          46     46
FT   TURN          47     49
FT   STRAND        50     52
FT   STRAND        57     58
FT   STRAND        60     65
FT   STRAND        72     73
FT   STRAND        79     84
FT   HELIX         86     90
FT   TURN          91     93
FT   STRAND        93     93
FT   STRAND        99    104
FT   STRAND       107    108
FT   TURN         111    116
FT   STRAND       124    125
FT   TURN         131    132
FT   STRAND       134    139
FT   HELIX        145    147
FT   TURN         148    149
FT   STRAND       152    152
FT   TURN         154    154
FT   TURN         154    154
FT   HELIX        155    158
FT   TURN         162    166
SQ   SEQUENCE     336 AA;  37202 MW;  D08949996E399554 CRC64;
```

```
Query Match             25.7%;   Score 628.5;  DB 1;  Length 336;
Best Local Similarity   41.8%;   Pred. No. 1.4e-32;
Matches 137;  Conservative 49;  Mismatches 129;  Indels 13;  Gaps 5;

Qy      14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPGPHSS 73
           |:|:|    ||||||||||:||||:||||||||||:|||||
Db      17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73

Qy      74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
           |:|:|    :||:|    |:|:|||:||||||||||||||||:|:|    ||:|||:||
Db      74 GQYEYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133

Qy     134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
           ||||    :|:|    |:|||||||||||:|||    ||||||:|||:||||||    |
Db     134 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

Qy     191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
           |||    :||:|    ||||:||:|    |:|||:|    ||:||||||||:||||||
Db     194 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIFIVIIITLVVLLL 253

Qy     251 WRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
           ||||:|    |:|||    :|    :|    ||:|    |:||||    ||||    ||
Db     254 KYRRHRKHSPQHTTTLSLSTLATPKRGGNN---NGSEPSDVIIPLR---TADSVFCPH 306

Qy     311 YEKVSGDYGHPVYIVQDGPPQSPPNIIY 338
           ||||||||||||:||:||||||||||||
Db     307 YEKVSGDYGHPVIVQEMPPQSPANIIY 334
```

OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Ebert L., Muenstermann E., Schatten R., Henze S., Bohn E.,
RA   Mollenhauer J., Wiemann S., Schick M., Korn B.;
RT   "Cloning of mouse full open reading frames in Gateway(R) system entry
RT   vector (pDONR201).";
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; CT010381; CAJ18588.1; -; mRNA.
SQ   SEQUENCE   336 AA; 37202 MW; D08949996E399554 CRC64;

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Query Match             25.7%;   Score 628.5;  DB 2;  Length 336;
Best Local Similarity   41.8%;   Pred. No. 1.4e-32;
Matches 137;  Conservative 49;  Mismatches 129;  Indels 13;  Gaps 5;

Qy      14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPGPHSS 73
           |:|:|    ||||||||||:||||:||||||||||:|||||
Db      17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73

Qy      74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
           |:|:|    :||:|    |:|:|||:||||||||||||||||:|:|    ||:|||:||
Db      74 GQYEYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133

Qy     134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
           ||||    :|:|    |:|||||||||||:|||    ||||||:|||:||||||    |
Db     134 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

Qy     191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
           |||    :||:|    ||||:||:|    |:|||:|    ||:||||||||:||||||
Db     194 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIFIVIIITLVVLLL 253

Qy     251 WRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
           ||||:|    |:|||    :|    :|    ||:|    |:||||    ||||    ||
Db     254 KYRRHRKHSPQHTTTLSLSTLATPKRGGNN---NGSEPSDVIIPLR---TADSVFCPH 306

Qy     311 YEKVSGDYGHPVYIVQDGPPQSPPNIIY 338
           ||||||||||||:||:||||||||||||
Db     307 YEKVSGDYGHPVIVQEMPPQSPANIIY 334
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RT   membrane attachment or clustering for activity.";
RL   Science 266:816-819(1994).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RA   Fletcher F.A., Huebner K., Shaffer L.G., Monaco A., Mueller U.,
RA   Kozlosky C., Druck T., Simoneaux D.K., Fairweather N., Chelly J.,
RA   Cerretti D.P., Belmont J.W., Beckmann M.P., Lyman S.D.;
RT   "Assignment of the human Elk ligand gene, EPLG2, to chromosome region
RT   Xq12.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15772651; DOI=10.1038/nature03440;
RA   Ross M.T., Grafham D.V., Coffey A.J., Scherer S., McLay K., Muzny D.,
RA   Platzer M., Howell G.R., Burrows C., Bird C.P., Frankish A.,
RA   Lovell F.L., Howe K.L., Ashurst J.L., Fulton R.S., Sudbrak R., Wen G.,
RA   Jones M.C., Hurles M.E., Andrews T.D., Scott C.E., Searle S., Chen R.,
RA   Ramser J., Whittaker A., Deadman R., Carter N.P., Hunt S.E., Chen R.,
RA   Cree A., Gunaratne P., Havlak P., Hodgson A., Metzker M.L.,
RA   Richards S., Scott G., Steffen D., Sodergren E., Wheeler D.A.,
RA   Worley K.C., Ainscough R., Ambrose K.D., Ansari-Lari M.A., Aradhya S.,
RA   Ashwell R.I., Babbage A.K., Bagguley C.L., Ballabio A., Banerjee R.,
RA   Barker G.E., Barlow K.F., Barrett I.P., Bates K.N., Beare D.M.,
RA   Beasley H., Beasley O., Beck A., Bethel G., Blechschmidt K., Brady N.,
RA   Bray-Allen S., Bridgeman A.M., Brown A.J., Brown M.J., Bonnin D.,
RA   Bruford E.A., Buhay C., Burch P., Burford D., Burgess J., Burrill W.,
RA   Burton J., Bye J.M., Carder C., Carrel L., Chako J., Chapman J.C.,
RA   Chavez D., Chen E., Chen G., Chen Y., Chen Z., Chinault C.,
RA   Ciccodicola A., Clark S.Y., Clarke G., Clee C.M., Clegg S.,
RA   Clerc-Blankenburg K., Clifford K., Cobley V., Cole C.G., Conquer J.S.,
RA   Corby N., Connor R.E., David R., Davies J., Davis C., Davis J.,
RA   Delgado O., Deshazo D., Dhami P., Ding Y., Dinh H., Dodsworth S.,
RA   Draper H., Dugan-Rocha S., Dunham A., Dunn M., Durbin K.J., Dutta I.,
RA   Eades T., Ellwood M., Emery-Cohen A., Errington H., Evans K.L.,
RA   Faulkner L., Francis F., Frankland J., Fraser A.E., Galgoczy P.,
RA   Gilbert J., Gill R., Gloeckner G., Gregory S.G., Gribble S.,
RA   Griffiths C., Grocock R., Gu Y., Gwilliam R., Hamilton C., Hart E.A.,
RA   Hawes A., Heath P.D., Heitmann K., Hennig S., Hernandez J.,
RA   Hinzmann B., Ho S., Hoffs M., Howden P.J., Huckle E.J., Hume J.,
RA   Hunt P.J., Hunt A.R., Isherwood J., Jacob L., Johnson D., Jones S.,
RA   de Jong P.J., Joseph S.S., Keenan S., Kelly S., Kershaw J.K., Khan Z.,
RA   Kioschis P., Klages S., Knights A.J., Kosiura A., Kovar-Smith C.,
RA   Laird G.K., Langford C., Lawlor S., Leversha M., Lewis L., Liu W.,
RA   Lloyd C., Lloyd D.M., Loulseged H., Loveland J.E., Lovell J.D.,
RA   Lozado R., Lu J., Lyne R., Ma J., Maheshwari M., Matthews L.H.,
RA   McDowall J., McLaren S., McMurray A., Meidl P., Meitinger T.,
RA   Milne S., Miner G., Mistry S.L., Morgan M., Morris S., Mueller I.,
RA   Mullikin J.C., Nguyen N., Nordsiek G., Nyakatura G., O'dell C.N.,
RA   Okwuonu G., Palmer S., Pandian R., Parker D., Parrish J.,
RA   Pasternak S., Patel D., Pearce A.V., Pearson D.M., Pelan S.E.,
RA   Perez L., Porter K.M., Ramsey Y., Reichwald K., Rhodes S.,
RA   Ridler K.A., Schlessinger D., Schueler M.G., Sehra H.K.,
RA   Shaw-Smith C., Shen H., Sheridan E.M., Shownkeen R., Skuce C.D.,
RA   Smith M.L., Sotheran E.C., Steingruber H.E., Steward C.A., Storey R.,
RA   Swann R.M., Swarbreck D., Tabor P.E., Taudien S., Taylor T.,
RA   Teague B., Thomas K., Thorpe A., Timms K., Tracey A., Trevanion S.,
RA   Tromans A.C., d'Urso M., Verduzco D., Villasana D., Waldron L.,
RA   Wall M., Wang Q., Warren J., Warry G.L., Wei X., West A.,
RA   Whitehead S.L., Whiteley M.N., Wilkinson J.E., Willey D.L.,
RA   Williams G., Williams L., Williamson A., Williamson H., Wilming L.,
RA   Woodmansey R.L., Wray P.W., Yen J., Zhang J., Zhou J., Zoghbi H.,
RA   Zorilla S., Buck D., Reinhardt R., Poustka A., Rosenthal A.,
RA   Lehrach H., Meindl A., Minx P.J., Hillier L.W., Willard H.F.,
RA   Wilson R.K., Waterston R.H., Rice C.M., Vaudin M., Coulson A.,
RA   Nelson D.L., Weinstock G., Sulston J.E., Durbin R., Hubbard T.,
RA   Gibbs R.A., Beck S., Rogers J., Bentley D.R.;
RT   "The DNA sequence of the human X chromosome.";
RL   Nature 434:325-337(2005).
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   PROTEIN SEQUENCE OF 28-42.
RX   PubMed=15340161; DOI=10.1110/ps.04682504;
RA   Zhang Z., Henzel W.J.;
RT   "Signal peptide prediction based on analysis of experimentally
RT   verified cleavage sites.";
RL   Protein Sci. 13:2819-2824(2004).
RN   [7]
RP   INTERACTIONS WITH GRIP1 AND GRIP2.
RX   MEDLINE=99211388; PubMed=10197531; DOI=10.1016/S0896-6273(00)80706-0;
RA   Brueckner K., Pablo Labrador J., Scheffler P., Herb A., Seeburg P.H.,
RA   Klein R.;
RT   "EphrinB ligands recruit GRIP family PDZ adaptor proteins into raft
RT   membrane microdomains.";
RL   Neuron 22:511-524(1999).
RN   [8]
RP   VARIANTS CFNS LEU-54 AND ILE-111.
RX   PubMed=15124102; DOI=10.1086/421532;
RA   Wieland I., Jakubiczka S., Muschke P., Cohen M., Thiele H.,
RA   Gerlach K.L., Adams R.H., Wieacker P.;
RT   "Mutations of the ephrin-B1 gene cause craniofrontonasal syndrome.";
RL   Am. J. Hum. Genet. 74:1209-1215(2004).
RN   [9]
RP   VARIANTS CFNS THR-62; SER-98; PRO-115; HIS-119; THR-119; SER-151;
RP   VAL-151; PRO-155; ILE-158 AND VAL-158; AND VARIANT HIS-154.
RX   PubMed=15162289; DOI=10.1073/pnas.0402819101;
RA   Twigg S.R.F., Kan R., Babbs C., Bochukova E.G., Robertson S.P.,
RA   Wall S.A., Morriss-Kay G.M., Wilkie A.O.M.;
RT   "Mutations of ephrin-B1 (EFNB1), a marker of tissue boundary
RT   formation, cause craniofrontonasal syndrome.";
RL   Proc. Natl. Acad. Sci. U.S.A. 101:8652-8657(2004).
RN   [10]
RP   VARIANTS CFNS ARG-27; LEU-54; SER-119; HIS-119; ALA-137; PHE-138;
RP   SER-151; SER-153; TYR-153 AND ARG-182.
RX   PubMed=15959873; DOI=10.1002/humu.20193;
RA   Wieland I., Reardon W., Jakubiczka S., Franco B., Kress W.,
RA   Vincent-Delorme C., Thierry P., Edwards M., Koenig R., Rusu C.,
RA   Schweiger S., Thompson E., Tinschert S., Stewart F., Wieacker P.;
RT   "Twenty-six novel EFNB1 mutations in familial and sporadic
RT   craniofrontonasal syndrome (CFNS).";
RL   Hum. Mutat. 26:1-6(2005).
CC   -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB1 and EPHA1.
CC   Binds to, and induce the collapse of, commissural axons/growth
CC   cones in vitro. May play a role in constraining the orientation of
CC   longitudinally projecting axons (By similarity).
CC   -!- SUBUNIT: Interacts with GRIP1 and GRIP2.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Heart, placenta, lung, liver, skeletal muscle,
CC   kidney, pancreas.
CC   -!- INDUCTION: By TNF-alpha.
CC   -!- PTM: Inducible phosphorylation of tyrosine residues in the
CC   cytoplasmic domain (By similarity).
CC   -!- DISEASE: Defects in EFNB1 are a cause of craniofrontonasal

```
CC   syndrome (CFNS) [MIM:304110]; also known as craniofrontonasal
CC   dysplasia (CFND). CFNS is an X-linked inherited syndrome
CC   characterized by hypertelorism, coronal synostosis with
CC   brachycephaly, downslanting palpebral fissures, clefting of the
CC   nasal tip, joint anomalies, longitudinally grooved fingernails and
CC   other digital anomalies.
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; U09304; AAA53093.1; -; mRNA.
DR   EMBL; L37361; AAA52369.1; -; mRNA.
DR   EMBL; U09303; AAB41127.1; -; mRNA.
DR   EMBL; AL136092; CAB86409.1; -; Genomic_DNA.
DR   EMBL; BC016649; AAH16649.1; -; mRNA.
DR   EMBL; BC052979; AAH52979.1; -; mRNA.
DR   PIR; S46993; S46993.
DR   HSSP; P52800; 1IKO.
DR   Ensembl; ENSG00000090776; Homo sapiens.
DR   HGNC; HGNC:3226; EFNB1.
DR   H-InvDB; HIX0016846; -.

Query Match             39.2%;  Score 623;  DB 1;  Length 346;
Best Local Similarity   25.4%;
Matches  143;  Conservative   48;  Pred. No. 3.2e-32;  Mismatches 116;  Indels 58;  Gaps  9;

Qy       8 PGGVRVGALLLLGVLGLVSGL--------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
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Db       4 PGQRWLGKWLVAMVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy      62 CPRARPPGPHSSSPNYEFYXLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
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Db      64 CPRAEAGRP-----YEYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQSIRFTIKFQEFS 118

Qy     122 PNLWGHEFRSHHDYYIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
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Db     119 PNYMGLEFKKHHDYYITSTNGSLEGLENREGGVCRTRTMKIIMKVGQDPNAVTPEQLTT 178

Qy     182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGLA---- 236
           :   || |  |  |   | | |  ||:  :   || |||  :  |:
Db     179 SRPSKEADNTVKMATQAPSGRSLGDSDGHETVNQEEKSGP------GASGSSSGDPD 231

Qy     237 -----LILLGVAGGA------------MCWRRRAKPSESRHPGPGSFGRGGSLGL 277
                : | |  ||                     : || | :  | :|| | :|
Db     232 GFENSKVALFAAVGAGCVTFLLIIIFLIVLLLKLRKRHKHTQQ-----RAAALSL 282

Qy     278 ----GGGGGMGPREAEPGELGIALRGGGAADPPPCPHYEKVSGDYGHPVIVQDGPPQSP 333
                |||  |    |   |     | ::   | |||||||||||||||||| ||: ||||
Db     283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339

Qy     334 PNIYY 338
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Db     340 ANIYY 344
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RESULT 10

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ID   EFNB2_HUMAN     STANDARD;      PRT;   333 AA.
AC   P52799;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ephrin-B2 precursor (EPH-related receptor tyrosine kinase ligand 5)
DE   (LERK-5) (HTK ligand)
GN   Name=EFNB2; Synonyms=EPLG5, HTKL, LERK5;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
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OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=95199254; PubMed=7534404;
RA   Bennett B.D., Zeigler F.C., Gu Q., Fendly B., Goddard A.D.,
RA   Gillett N., Matthews W.;
RT   "Molecular cloning of a ligand for the EPH-related receptor protein-
RT   tyrosine kinase Htk.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:1866-1870(1995).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=96145238; PubMed=8559144; DOI=10.1016/0161-5890(95)00108-5;
RA   Cerretti D.P., Vanden Bos T., Nelson N., Kozlosky C.J., Reddy P.,
RA   Maraskovsky E., Park L.S., Lyman S.D., Copeland N.G., Gilbert D.J.,
RA   Jenkins N.A., Fletcher F.A.;
RT   "Isolation of LERK-5: a ligand of the eph-related receptor tyrosine
RT   kinases.";
RL   Mol. Immunol. 32:1197-1205(1995).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   MEDLINE=98192220; PubMed=9535549;
RA   Vogt T., Stolz W., Welsh J., Jung B., Kerbel R.S., Kobayashi H.,
RA   Landthaler M., McClelland M.;
RT   "Overexpression of Lerk-5/Eplg5 messenger RNA: a novel marker for
RT   increased tumorigenicity and metastatic potential in human malignant
RT   melanomas.";
RL   Clin. Cancer Res. 4:791-797(1998).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB4 and EPHA3.
CC       May play a role in constraining the orientation of longitudinally
CC       projecting axons (By similarity).
CC   -!- SUBUNIT: Interacts with PDZRN3 (By similarity). Binds to the
CC       receptor tyrosine kinases EPHB4 and EPHA3.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Lung and kidney.
CC   -!- PTM: Inducible phosphorylation of tyrosine residues in the
CC       cytoplasmic domain (By similarity).
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC   ----------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ----------------------------------------------------------------------
DR   EMBL; U16797; AAA99707.1; -; mRNA.
DR   EMBL; L37734; AAC41752.1; -; mRNA.
DR   EMBL; U81262; AAD03786.1; -; mRNA.
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DR   EMBL; BC069342; AAH69342.1; -; mRNA.
DR   EMBL; BC074856; AAH74856.1; -; mRNA.
DR   EMBL; BC074857; AAH74857.1; -; mRNA.
DR   PIR; I84743; I84743.
DR   SMR; P52799; 27-167.
DR   HSSP; P52800; 1IKO.
DR   Ensembl; ENSG00000125266; Homo sapiens.
DR   HGNC; HGNC:3227; EFNB2.
MIM; 600527;;
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   GO; GO:0005886; C:plasma membrane; TAS.
DR   GO; GO:0046875; F:ephrin receptor binding; TAS.
DR   GO; GO:0001299; F:ephrin.
DR   GO; GO:0007267; P:cell-cell signaling; TAS.
DR   GO; GO:0009653; P:morphogenesis; TAS.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Differentiation; Glycoprotein; Neurogenesis;
KW   Phosphorylation; Signal; Transmembrane.
FT   SIGNAL        1     27       Potential.
FT   CHAIN        28    333       Ephrin-B2.
FT   TOPO_DOM     28    229       Extracellular (Potential).
FT   TRANSMEM    230    250       Potential.
FT   TOPO_DOM    251    333       Cytoplasmic (Potential).
FT   MOTIF       331    333       PDZ recognition motif (Potential).
FT   CARBOHYD     36     36       N-linked (GlcNAc...) (Potential).
FT   CARBOHYD    139    139       N-linked (GlcNAc...) (Potential).
FT   DISULFID     62    101       By similarity.
FT   DISULFID     89    153       By similarity.
SQ   SEQUENCE   333 AA;  36923 MW;  6D9932A632626AEA CRC64;

Query Match             25.3%;
Best Local Similarity   40.5%;
Matches  133;  Conservative   52;  Mismatches 130;  Indels  13;  Gaps   5;
                                    Score 620.5;  DB 1;  Length 333;

Qy         14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGHSS 73
              ::|                ||:| |||||||||:||:||||
Db         14 GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

Qy         74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
              ||:|| || |: : :| ::|    |  | :|  :||  ||||||||:|||||| || ::
Db         71 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy        134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPER-DR 190
              |||| ||::|: |||::| :|||| ||:||:|:|||    |:|        ::|||| ||
Db        131 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy        191 GAAHSLEPGKENLPGDPPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGAMC 250
              | ::|  |::::| | ::||:       || | :  | :::   |::|  :||  | | :
Db        191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCCIIFIVIIILVVLLL 250

Qy        251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
              ||:| | | : | |  :: ::    |:   |  :|:  :|  : :  | | ||| |||
Db        251 KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303

Qy        311 YEKVSGDYGHPVIVQDGPPQSPPNIYY 338
              |||||||||||||||: ||||| |||
Db        304 YEKVSGDYGHPVIVQEMPPQSPANIYY 331
```

```
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Dunn M.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL138689; CAI39907.1; -; Genomic_DNA.
DR   GO; GO:0016020; C:membrane; IEA.
NON_TER
SQ   SEQUENCE   333 AA;  36923 MW;  6D9932A632626AEA CRC64;

Query Match             25.3%;
Best Local Similarity   40.5%;
Matches  133;  Conservative   52;  Mismatches 130;  Indels  13;  Gaps   5;
                                    Score 620.5;  DB 2;  Length 333;

Qy         14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGHSS 73
              ::|                ||:| |||||||||:||:||||
Db         14 GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

Qy         74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
              ||:|| || |: : :| ::|    |  | :|  :||  ||||||||:|||||| || ::
Db         71 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy        134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPER-DR 190
              |||| ||::|: |||::| :|||| ||:||:|:|||    |:|        ::|||| ||
Db        131 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy        191 GAAHSLEPGKENLPGDPPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGAMC 250
              | ::|  |::::| | ::||:       || | :  | :::   |::|  :||  | | :
Db        191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCCIIFIVIIILVVLLL 250

Qy        251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
              ||:| | | : | |  :: ::    |:   |  :|:  :|  : :  | | ||| |||
Db        251 KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303

Qy        311 YEKVSGDYGHPVIVQDGPPQSPPNIYY 338
              |||||||||||||||: ||||| |||
Db        304 YEKVSGDYGHPVIVQEMPPQSPANIYY 331
```

RESULT 11
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ID   Q5JV56_HUMAN
AC   Q5JV56;
DT   10-MAY-2005 (TrEMBLrel. 30, Created)
DT   10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT   10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE   Ephrin-B2 (Fragment).
GN   Name=EFNB2; ORFNames=RP11-272L14.1-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

ID   Q5JV56_HUMAN PRELIMINARY;   PRT;   333 AA.

RESULT 12
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ID   Q9PU74_CHICK
AC   Q9PU74;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ephrin-B2 precursor.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Menzel P., Pasquale E.B.;
RT   "Coding sequence of chicken ephrin-B2.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF180729; AAD53948.1; -; mRNA.
DR   SMR; Q9PU74; 29-169.
DR   HSSP; P52800; 1IKO.
DR   Ensembl; ENSGALG00000016856; Gallus gallus.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Signal.
FT   SIGNAL        1     27       Potential.
FT   CHAIN        28    333       ephrin-B2.
SQ   SEQUENCE   333 AA;  36761 MW;  4C28E8CB21B7783 CRC64;
```

ID   Q9PU74_CHICK PRELIMINARY;   PRT;   333 AA.

RESULT 13

```
Query Match
Best Local Similarity   40.2%;  Score 620.5; DB 2; Length 333;
Matches    133;  Conservative  52; Mismatches 125; Indels  21; Gaps  6;

Qy   14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPGPHSS   73
         |||:|||||||||:|| ||:||::||  ||||:|||||||||||||||||  ||
Db   16 GALMLVMRTALAKSIVLDPIYWNSSNPKFLPGGQLVLYPQIGDKLDIICPKV---DSKTV   72

Qy   74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH  133
Db   73 GQYEYYKYMVDKDQADSCAIRKDNTPLLNCAKPDQDVKFTIKFQEFSPNLWGLEFQKNK   132

Qy  134 DYYIIATSDGTRREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMER-----  188
Db  133 DYYVISTNGSLEGLNNQEGGVCQTKTMKILMKVGQDENSAGLPR---STDPTKRPEQEA   189

Qy  189 -DRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAGAGGLALLLLGVAGAGG  247
Db  190 GTNGKSSTTSPVKDHGGSSTDG--SKAGHSSIIGSEVALFAGIASGGCIFIVIILLVV    247

Qy  248 AMCWRRRRAKPSESRHPGPGSFGRGGSIGLGGGGGMGPREAEPGELGIALRGGGAADPPF   307
Db  248 LLLKYRHRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVF   300

Qy  308 CPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY   338
Db  301 CPHYEKVSGDYGHPVYIVQEMPPQSPANIYY   331
```

EFNB1_CHICK

```
ID   EFNB1_CHICK     STANDARD;      PRT;   334 AA.
AC   O73612;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ephrin-B1 precursor (CEK5 ligand) (CEL5-L).
GN   Name=EFNB1;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=97223524; PubMed=9070326; DOI=10.1006/dbio.1996.8496;
RA   Holash J.A., Soans C., Chong L.D., Shao H., Dixit V.M., Pasquale E.B.;
RT   "Reciprocal expression of the Eph receptor Cek5 and its ligand(s) in
RT   the early retina.";
RL   Dev. Biol. 182:256-269(1997).
CC   -!- SUBUNIT: Binds to the receptor tyrosine kinase EPHB2. Interacts
CC       with GRIP1 and GRIP2 (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: Inducible phosphorylation of tyrosine residues in the
CC       cytoplasmic domain (By similarity).
CC   -!- SIMILARITY: Belongs to the ephrin family.
CC   --------------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   --------------------------------------------------------------------------
DR   EMBL; U72394; AAC07986.1; -; mRNA.
DR   HSSP; P52800; 1IKO.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Differentiation; Glycoprotein; Neurogenesis;
KW   Phosphorylation; Signal; Transmembrane.
FT   SIGNAL        1     25
FT   CHAIN        26    334       Ephrin-B1.
FT   TOPO_DOM     26    231       Extracellular (Potential).
FT   TRANSMEM    232    252       Potential.
FT   TOPO_DOM    253    334       Cytoplasmic (Potential).
FT   MOTIF       332    334       PDZ recognition motif (Potential).
FT   CARBOHYD    135    135       N-linked (GlcNAc...) (Potential).
FT   DISULFID     60     97       By similarity.
FT   DISULFID     85    149       By similarity.
SQ   SEQUENCE   334 AA;  36859 MW;  48AF56E9BD56CD5 CRC64;
```

RESULT 14

```
Query Match
Best Local Similarity   39.3%;  Score 619; DB 1; Length 334;
Matches    144;  Conservative  50; Mismatches 100; Indels  72; Gaps 13;

Qy    8 PGGVR--VGALLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRA    65
         :||     ||||||||||||||:|| |||||:|||||  ||||:|||||||||||:||
Db    4 PRGGRWLLGVLLALCRLAAPLAKSLEPVSWNSAGNPKFMSGKGLVIYPEIGDKLDIICPKA    63

Qy   66 RPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLW   125
         :||      ||||||||||:: | |: |||: | : |||||:  :|||||||||||:: |
Db   64 EPSKP----YDYKLYLVKKDQDADCSTVMDPNVLVTCNRPEQEIRFTIKFQEFSPNYM    118

Qy  126 GHEFRSHHDYYIIATSDGTRREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMP  185
         | |||: ||| | |:|| | |||: | |||||||||||||||| | |  |:||  :|| |
Db  119 GLEFKRQQDYFITSTNGTLDGLENRGGVCQTRSMKIVMKVGQDP-NAVIPEQLTTSRP    177

Qy  186 MER------------DRGAAHSL----EPGKENLPGDPTSNA--TSRGAEGPLPPPSMPAVAGA  232
         |:|           |||||||     ||||||||||||:||   ||||||||| ||:| |||
Db  178 SKEADNTVKLVTQSPRHKVPTVEBPGCK---PGSVNQNGQETQGPSDGFL--SSKVAVFAA    232

Qy  232 AGG----------LALLLLGVAGAGGAMCWRRRRAKPSESRH------PGPGSFGRG       272
         |||          |||||||:||||||||||||||||||||      |||||||
Db  233 IGACGVIFILIIFLVVLLIKI-----RKHRHRKHTQQRAAALSLSTLASPKCSGNA      283

Qy  273 GSLGLGGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQS   332
         ||||||||||||||||||||||||||||||||| ||||||||||||||||||||:|||||
Db  284 GS------------EPSDIIIPLR--TTENNYCPHYEKVSGDYGHPVYIVQEMPPQS     326

Qy  333 PPNIYY   338
Db  327 PANIYY   332
```

EFNB2_BRARE

```
ID   EFNB2_BRARE     STANDARD;      PRT;   332 AA.
AC   O73874;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   10-MAY-2005 (Rel. 47, Last annotation update)
DE   Ephrin-B2a precursor.
GN   Name=efnb2a; Synonyms=efnb2;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=98438455; PubMed=9765210;
RA   Durbin L., Brennan C., Shiomi K., Cooke J., Barrios A.,
RA   Shanmugalingam S., Guthrie B., Lindberg R., Holder N.;
RT   "Eph signaling is required for segmentation and differentiation of the
RT   somites.";
RL   Genes Dev. 12:3096-3109(1998).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21290827; PubMed=11397014; DOI=10.1006/dbio.2001.0281;
RA   Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
RA   Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;
RT   "Morphogenesis of prechordal plate and notochord requires intact
RT   eph/ephrin b signaling.";
```

RESULT 15
Q90Z33_BRARE
ID   Q90Z33_BRARE PRELIMINARY;   PRT;   341 AA.
AC   Q90Z33;

DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ephrin B1.
GN   Name=efnb1;
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21290827; PubMed=11397014; DOI=10.1006/dbio.2001.0281;
RA   Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
RA   Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;
RT   "Morphogenesis of prechordal plate and notochord requires intact
RT   eph/ephrin b signaling.";
RL   Dev. Biol. 234:470-482(2001).
DR   EMBL; AF375224; AAK64274.1; -; mRNA.
DR   HSSP; P52800; 1IKO.
DR   Ensembl; ENSDARG00000007723; Danio rerio.
DR   ZFIN; ZDB-GENE-010618-2; efnb1.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
SQ   SEQUENCE   341 AA; 37849 MW; CB922F20B0D93E94 CRC64;

Query Match   24.8%;
Best Local Similarity   41.5%;
Matches 139; Conservative 49; Mismatches 109; Indels 38; Gaps 11;

```
Qy   24 LVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGHSSPNYEFYKLYL 83
Db   23 LPAAKSLESVVWNSQNPKFVSGKGLVIYPBIGDKDIICPK----GDMGRP-YEFYKLYL 77

Qy   84 VGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDG 143
Db   78 VKKEQAESCCSTILDPNVLLVTCNKPEKDIKFTIKFQEFSENYMGLEFKRFTNYYITSTSNG 137

Qy  144 TREGLESLQGGVCLTRGMKVLLRVGQSPRG-----GAVPRKPVSEMPMERDRGAAHSLEP 198
Db  138 TQEGLENREGGVCSTRSMKIIMKVGQDPNAPDDPLPDLLPDRPYDNEIKDPTTSPSRKTER 197

Qy  199 GKEN------LPGDPTSNATSR--GAEGPLPPSMPAVAGAAG--GLALLLLGVAGAGG 247
Db  198 GRENEVDGNGSKMPGKDTRNQNNSPGSVEGIF--GSKPALPAALGAGCVIFLLIIIILIV 255

Qy  248 AMCWRRRRAKPSESRHPGPGSFGRGGGSL-----GLGGGGMGPREAEPGELGIALRGGGAA 303
Db  256 LLIKLRKTR----XHSQP----RGGTALSLSTLATPKGAAQAGSEPSDIIIPLR---TT 304

Qy  304 DPPPCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
Db  305 ENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYY 339
```

Search completed: December 21, 2005, 14:35:33
Job time : 181.277 secs

RL   Dev. Biol. 234:470-482(2001).
CC   -!- SUBUNIT: Binds to the receptor tyrosine kinase EPHB4.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- PTM: Inducible phosphorylation of tyrosine residues in the
CC   cytoplasmic domain (By similarity).
CC   -!- SIMILARITY: Belongs to the ephrin family.
DR   EMBL; AJ004863; CAA06168.1; -; mRNA.
DR   EMBL; AF375225; AAK64275.1; -; mRNA.
DR   HSSP; P52800; 1IKO.
DR   Ensembl; ENSDARG00000020164; Danio rerio.
DR   ZFIN; ZDB-GENE-990415-67; efnb2a.
DR   GO; GO:0008039; P:synaptic target recognition; IEP.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
DR   PROSITE; PS01299; EPHRIN; 1.
KW   Developmental protein; Differentiation; Glycoprotein; Neurogenesis;
KW   Phosphorylation; Signal; Transmembrane.
FT   SIGNAL   1   24   Potential.
FT   CHAIN   25   332   Ephrin-B2a.
FT   TOPO_DOM   25   225   Extracellular (Potential).
FT   TRANSMEM   226   246   Potential.
FT   TOPO_DOM   247   332   Cytoplasmic (Potential).
FT   MOTIF   330   332   PDZ recognition motif (Potential).
FT   CARBOHYD   20   20   N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   33   33   N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   136   136   N-linked (GlcNAc...) (Potential).
FT   CARBOHYD   211   211   N-linked (GlcNAc...) (Potential).
FT   DISULFID   59   98   By similarity.
FT   DISULFID   86   150   By similarity.
SQ   SEQUENCE   332 AA; 36724 MW; 189ED82372C71C8B CRC64;

Query Match   25.2%;
Best Local Similarity   41.8%;
Matches 143; Conservative 54; Mismatches 106; Indels 39; Gaps 12;

```
Qy   14 GALLLLGVILGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGHSS 73
Db   11 GVLVIACKVNLSRALILDSIYWNTNTNTKFVPGQQLVLYPQIGDKMDIVCPRVE---GGSM 67

Qy   74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
Db   68 EGVEVYKLYMVPLEQLKSCQVTKADTPLLNCVRPDQDVKFTLKFQEFSPNIWGLEFRGK 127

Qy  134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK-PVSEMPMERDRGA 192
Db  128 DYYIISTSNGTMEGLDNQEGGVCKTKSMKIIMKVGQNPSDPISPKDYPTSYPPKHPDLGG 187

Qy  193 AHS------LEP----GKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGV 242
Db  188 KDSKSNEVLKPDASPHGEDK--GDGNKSSSVIGSEVAL----FACIASASVIVIIIIIML 241

Qy  243 AGAGGAMCWRRRRAKPSESRHPGPGSFG------RGGSLGLGGGGGMGPREAEPGELGIA 296
Db  242 VFL--LLKYRHRKHS-PQHATTLSLSTLIATPKRGGS----GGNNNG---SEPSDIIIP 291

Qy  297 LRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
Db  292 LR--TADSVFCPHYEKVSGDYGHPVYIVQEMPPQSPANIYY 330
```

OM protein - protein search, using sw model

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GenCore version 5.1.6

Run on: December 21, 2005, 14:36:40 ; Search time 8.58491 Seconds
                                                (without alignments)
                                                378.002 Million cell updates/sec

Title: US-10-021-121-2
Perfect score: 2450
Sequence: 1 MGPPHSGPGGVRVGALLLLG...........TTLLRQRASVEAEACQHGPL 455

Scoring table: BLOSUM62
             Gapop 10.0 , Gapext 0.5

Searched: 53982 seqs, 7132107 residues
Total number of hits satisfying chosen parameters: 53982

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA_New:*
               1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
               2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
               3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
               4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
               5: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep:*
               6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
               7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
               8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	620.5	25.3	333	6	US-10-949-720-396	Sequence 396, App
2	451.5	18.4	459	6	US-10-949-720-390	Sequence 390, App
3	442	18.0	233	6	US-10-995-561-990	Sequence 390, App
4	164.5	6.7	204	6	US-10-131-826A-288	Sequence 288, App
5	144.5	5.9	1516	6	US-10-220-824-8	Sequence 8, Appli
6	142.5	5.8	1496	7	US-11-186-284-35	Sequence 35, Appl
7	142	5.8	744	7	US-11-186-284-37	Sequence 37, Appl
8	142	5.8	744	7	US-11-186-284-39	Sequence 39, Appl
9	141.5	5.8	1166	6	US-10-821-234-964	Sequence 964, App
10	141.5	5.8	1166	6	US-10-821-234-33	Sequence 33, Appl
11	137.5	5.6	1466	7	US-11-186-284-33	Sequence 33, Appl
12	135.5	5.5	1874	6	US-10-821-234-1182	Sequence 1182, Ap
13	134.5	5.5	1532	6	US-10-821-234-914	Sequence 914, App
14	134.5	5.5	1366	6	US-10-821-234-1431	Sequence 1431, Ap
15	134.5	5.5	1366	7	US-11-186-284-31	Sequence 31, Appl
16	134.5	5.5	1366	7	US-11-186-284-28	Sequence 28, Appl
17	134.5	.4	1464	7	US-11-186-284-28	Sequence 28, Appl
18	134	.4	1467	7	US-10-821-234-1096	Sequence 1096, Ap
19	134	.4	1464	7	US-11-000-463-243	Sequence 243, App
20	134	.4	1767	6	US-10-995-561-911	Sequence 911, App
21	134	.4	1767	6	US-10-995-561-914	Sequence 914, App
22	134	.4	1806	6	US-10-995-561-912	Sequence 912, App
23	134	.4	1806	6	US-10-995-561-915	Sequence 915, App
24	134	.4	1806	6	US-10-995-561-910	Sequence 910, App
25	134	.4	1818	6	US-10-995-561-913	Sequence 913, App
26	119	4.9	467	6	US-10-821-234-1688	Sequence 1688, Ap
27	116.5	4.8	1823	6	US-10-995-561-988	Sequence 988, App
28	116.5	4.8	2102	6	US-10-995-561-990	Sequence 990, App
29	116.5	4.8	2108	6	US-10-995-561-989	Sequence 989, App
30	116.5	4.8	2157	6	US-10-995-561-991	Sequence 991, App
31	114	4.7	828	6	US-10-995-561-983	Sequence 983, Appl
32	114	4.7	918	6	US-10-995-561-981	Sequence 981, App
33	114	4.7	1019	6	US-10-995-561-982	Sequence 982, App
34	113.5	4.6	580	6	US-10-995-561-987	Sequence 987, App
35	112	4.6	924	6	US-10-857-780-20	Sequence 20, Appli
36	111	4.5	641	6	US-10-477-507A-4	Sequence 4, Appli
37	107	4.4	924	7	US-10-848-976-1	Sequence 786, App
38	105.5	4.3	456	6	US-10-477-507A-2	Sequence 4, Appli
39	104.5	4.3	244	6	US-11-107-028-26	Sequence 26, Appli
40	103.5	4.2	884	6	US-11-102-240-16	Sequence 16, Appli
41	102	4.2	119	7	US-11-110-424-4	Sequence 4, Appli
42	101	4.1	673	7	US-11-451-375-12	Sequence 12, Appl
43	101	4.1	483	6	US-10-451-375-12	Sequence 12, Appl
44	101	4.1	1377	6	US-10-821-234-1070	Sequence 1070, Ap
45	99.5	4.1	368	7	US-11-085-775-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-10-949-720-396
; Sequence 396, Application US/10949720
; Publication No. US20050249736A1
; GENERAL INFORMATION:
; APPLICANT: Krasnoperov, Valery
; APPLICANT: Zozulya, Sergey
; APPLICANT: Kertesz, Nathalie
; APPLICANT: Reddy, Ramachandra
; APPLICANT: Gill, Parkash
; TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
; TITLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH
; FILE REFERENCE: VASG-P02-002
; CURRENT APPLICATION NUMBER: US/10/949,720
; CURRENT FILING DATE:
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: 60/454,432
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/454,300
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/454,300
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/800,350
; PRIOR FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 396
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-949-720-396

Query Match   25.3%; Score 620.5; DB 6; Length 333;
Best Local Similarity   40.5%; Pred. No. 6.8e-43;
Matches 133; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

Qy   14 GAILLLGVLGLVSGLSLEPYYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPGPHSS 73
             :| ||:::||::|||:||::|||:|| ||::|||:|||||||||::
Db   14 GVLMVLCRFAISKSIVLEPIYWNSSNSKFLPGGQGLVLYPQIGDKLDIICPKV--DSKTV 70

Qy   74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
             |:|||:|:|:|||::| |||:|:|||:||:
Db   71 GQYEYKVIMVDKDQQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy   134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPER-DR 190
             |||:|:||:| |:|:|:| :|:||| :||::|:
Db   131 DYYISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy   191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLGVAGAGGAMC 250
             | ::   : | :   ::   : :: : :: :| |
Db   191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGGCIFIVIIITLVVLLL 250

```
Qy    251 WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGGGAADPPPFCPH 310
          |||||||||||||||||| ||| :| :|:  |  :::|  ||||||||||  |||||| ||||
Db    251 KYRRRHRKHSPQHTTTLSLSTLAATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303

Qy    311 YEKVSGDYGHPVYIVQDGPQPSPPNIYY 338
          | :| :|  ||  :| |  ||||||||
Db    304 YEKVSGDYGHPVIVQEMPPQSPANIYY 331
```

RESULT 2
US-10-949-720-390

```
; Sequence 390, Application US/10949720
; Publication No. US20050249736A1
; GENERAL INFORMATION:
; APPLICANT: Krasnoperov, Valery
; APPLICANT: Zozulya, Sergey
; APPLICANT: Kertesz, Nathalie
; APPLICANT: Reddy, Ramachandra
; APPLICANT: Gill, Parkash
; TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
; TITLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH
; FILE REFERENCE: VASG-P02-002
; CURRENT APPLICATION NUMBER: US/10/949,720
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/454,432
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/454,300
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/800,350
; PRIOR FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 390
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Recombinant B2EC-FC protein
US-10-949-720-390
```

```
Query Match             18.4%;  Score 451.5;  DB 6;  Length 459;
Best Local Similarity   29.5%;  Pred. No. 3.3e-29;
Matches  122;  Conservative  47;  Mismatches  115;  Indels  129;  Gaps  11;

Qy     14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGHSS 73
          || :||                 ||||||||:|||||||| |||||||||||||||||::
Db     14 GVLMVLCRTAISKSIVLBPIYWNSSNSKRFLPGQGLVYLYPQIGDKLDIICPKV---DSKTV 70

Qy     74 PNYEFYKLYLVGGAQGRRCEAPAPANLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
          ||:|  |: |:|     ::||||||:|:||  |:  |: :|:|||||||||||  ::|:|
Db     71 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy    134 DYYIIATSDGTREGLESLQGGVCLLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAA 193
          |::||: |  ||:|   :|:|||| |  | :|::||::||| ::| |||  :||:|||
Db    131 DYYIISTNGSLEGLDNQEGGVCQTRAMKILMKVGQ-------------------------- 166

Qy    194 HSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAGAGGLALLLGVAGAGGAMCWRR 253
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    167 ------------------DASSAGSTRNKDPTRRPELE--------------AGTNG----- 191

Qy    254 RRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGIALRGGGAADP--------- 305
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    192 RSSTTSPVKPNPGSSTDGNSAGHSGNNILG-SEVDP----------------EPKSCDKTHT 237

Qy    306 -PFCPHYEKVSG------------------------------------------DYGH---- 323
          ||||||||||:|                                        |||
Db    238 CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWVDGVEVH 297

Qy    324 IVQDGPPQSPPNIYYTSISVLEWPILHTIQLFPMRSKCSRVTTFLFPVQVITT 376
          :|:|  |  ::||||:|:|::| :||:|:||  |: : |  |:|||:||| |
Db    298 NAKTKPREEQYNSTYRVVSVL--TVLHQDWLNGKEYKC-KVSNKALPAPIEKT 347
```

RESULT 3
US-10-949-720-388

```
; Sequence 388, Application US/10949720
; Publication No. US20050249736A1
; GENERAL INFORMATION:
; APPLICANT: Krasnoperov, Valery
; APPLICANT: Zozulya, Sergey
; APPLICANT: Kertesz, Nathalie
; APPLICANT: Reddy, Ramachandra
; APPLICANT: Gill, Parkash
; TITLE OF INVENTION: POLYPEPTIDE COMPOUNDS FOR INHIBITING
; TITLE OF INVENTION: ANGIOGENESIS AND TUMOR GROWTH
; FILE REFERENCE: VASG-P02-002
; CURRENT APPLICATION NUMBER: US/10/949,720
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/454,432
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 60/454,300
; PRIOR FILING DATE: 2003-03-12
; PRIOR APPLICATION NUMBER: US 10/800,350
; PRIOR FILING DATE: 2004-03-12
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 388
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Recombinant B2EC protein
US-10-949-720-388
```

```
Query Match             18.0%;  Score 442;  DB 6;  Length 233;
Best Local Similarity   35.8%;  Pred. No. 8.7e-29;
Matches   97;  Conservative  36;  Mismatches  76;  Indels  62;  Gaps  4;

Qy     14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGHSS 73
          || :||                 ||||||||:|||||||| |||||||||||||||||::
Db     14 GVLMVLCRTAISKSIVLBPIYWNSSNSKRFLPGQGLVYLYPQIGDKLDIICPKV---DSKTV 70

Qy     74 PNYEFYKLYLVGGAQGRRCEAPAPANLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
          ||:|  |: |:|     ::||||||:|:||  |:  |: :|:|||||||||||  ::|:|
Db     71 GQYEYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy    134 DYYIIATSDGTREGLESLQGGVCLLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAA 193
          |::||: |  ||:|   :|:|||| |  | :|::||::||| ::| |||  :||:|||
Db    131 DYYIISTNGSLEGLDNQEGGVCQTRAMKILMKVGQ-------------------------- 166

Qy    194 HSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAGAGGLALLLGVAGAGGAMCWRR 253
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    167 ------------------DASSAGSTRNKDPTRRPELE--------------AGTNG----- 191

Qy    254 RRAKPSESRHPGPGSFGRGGSLGLGGGGMG 284
          ||||||||||||||||||||||||||||||
Db    192 RSSTTSPVKPNPGSSTDGNSAGHSGNNILG 222
```

RESULT 4
US-10-131-826A-288

```
; Sequence 288, Application US/10131826A
; Publication No. US20050245730A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
```

; APPLICANT: Smith,Victoria
; APPLICANT: Stewart,Timothy A.
; APPLICANT: Tumas,Daniel
; APPLICANT: Watanabe,Colin K
; APPLICANT: Wood,William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C128
; CURRENT APPLICATION NUMBER: US/10/131,826A
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 288
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-131-826A-288

Query Match   5.9%; Score 144.5; DB 6; Length 1516;
Best Local Similarity   23.5%; Pred. No. 0.00049;
Matches 73; Conservative 18; Mismatches 82; Indels 137; Gaps 15;

Qy   52 PQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLYLGGAQGRRCEAPPAPNLLLTCDRPDLDL 111
              : |:| |||||
Db   620 PGVGER---------GPPGPGPP-------------------------GPPGPS------- 640

Qy   112 RFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGTRBG--LESLQGGVCLLTRGMKVLLRVGQ 169
                                       |:| | |||:|
Db   641 ---------------------FR--HDKLTFIDMBGSGFGGDLBALRG------------- 665

Qy   170 SPRGGAVPRKP--VSEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMP 226
                              ||::|: |||| ::| |
Db   666 -PRGPGPGPGPVGPLGGEPGRGVNSSDVPGAAGLPGVP-------GREGPGPFGPGLP 717

Qy   227 AVAGAAGGLALLLLGVAGGAGCWRRRAKPSESRHPGPGSFGRGGGSLGLGGGGMGPR 286
                                                     ||:|
Db   718 GPPGGPPG---------------------REGPGPGRTGQKGSLGEAGAPGHKGS 749

Qy   287 EAEPGELGIALRGG------GAADPPFCP------------HYEKVSGDYGHPVVIV--Q 326
              ::||| | | || ::| |
Db   750 KGAPGPAGARGESGGLAGAPGPAGPPGPGPPGPGPPGPGLPAGFDDMEGS-GGPFWSTARSA 808

Qy   327 DGPPQSPPNI 336
              || || |:
Db   809 DG-PQGPPGL 817

RESULT 6
US-11-186-284-35
; Sequence 35, Application US/11186284
; Publication No. US2005026493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US/10/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 1496
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-35

Query Match   5.8%; Score 142.5; DB 7; Length 1496;
Best Local Similarity   29.1%; Pred. No. 0.0007;
Matches 55; Conservative 15; Mismatches 76; Indels 43; Gaps 9;

Qy   169 QSPRG--GAV-PRKPVSEMPMERDRGAAHSLEPGKENLPG--------DPTSNATSRGAE 217

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-220-824-8

Query Match   6.7%; Score 164.5; DB 6; Length 204;
Best Local Similarity   27.7%; Pred. No. 1.2e-06;
Matches 46; Conservative 31; Mismatches 74; Indels 15; Gaps 5;

Qy   18 LLGVLGLVSGLSLEPVVWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS-PNY 76
              ||||||||| ||||| | |::| :: ||| | |||:::|||:||
Db   8 LLGLCCSLAAADRHTVFWNSSNPKFRNE-DYTIHVQLNDYVDIICPHYE---DHSADAAM 63

Qy   77 EFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHH 133
              ||| ||||| || ||||:| :| ||| |||:||| |:|| |||:||
Db   64 EQYILVLVEHERYQLCQPOSKDQVRWQCNRPSAKHGPEKLSEKFQRTPFTLGKEFKEGH 123

Qy   134 DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK 179
              |:|||| :| || | || | :|:| | :|:
Db   124 SYYISKPIHQHEDR----------CLRLKVTVSGKITHSPQAHDNPQE 162

RESULT 5
US-10-220-824-8
; Sequence 8, Application US/10220824
; Publication No. US2005027603A1
; GENERAL INFORMATION:
; APPLICANT: Viromed Limited
; TITLE OF INVENTION: Compositions for gene therapy of rheumatoid arthritis including a
; TITLE OF INVENTION: gene encoding an anti-angiogenic protein or parts thereof
; FILE REFERENCE: OPP0208/PCT
; CURRENT APPLICATION NUMBER: US/10/220,824
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: KR 2001-0000691
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Kopatentin 1.71
; SEQ ID NO 8
; LENGTH: 1516

```
Db   500 RGPRGDPGTLGPPGPVGERGAPGNRGF------PGSDGLPGPKGAQGERGPVGSSGPKGSQ 554
             :||||                         ||: ||| |  |         ||  :|:
Qy   218 GPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPGP----GSFGRGG 273

Db   555 GDPGRPGEPGLPGARG-----LTGNPGVQGPGEPGKLGPLGAPGEDGRPGPPGSIGIKGQPG 609
             ||: |                   :||        |::|
Qy   274 SLGLGGGGGMGPREAEPGELGIALRGGGAAADPPPCPHYEKVSGDYGHPVYIVQDGP--- 330

Db   610 TMGLPGPKGSNGDPGKPGEAG-----NPGVPGQRGAPGKDGKVGPYGPP-----GPPGLR 659
                                                                  :|||
Qy   331 ----QSPP 334

Db   660 GERGEQGPP 668
```

RESULT 7
US-11-186-284-37
; Sequence 37, Application US2005026493A1
; Publication No. US2005026493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 744
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-37

```
Query Match     5.8%;  Score 142;  DB 7;  Length 744;
Best Local Similarity   23.5%;  Pred. No. 0.00034;
Matches   73;  Conservative  16;  Mismatches  96;  Indels 126;  Gaps  14;

Qy    67 PPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWG 126
         |||||       |  :|     |         | |   |       :   |
Db   198 PPGPHGLPG------IGKPGGPLPGQPGPK----------------------------- 222

Qy   127 HEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPM 186
         :||                  |       |||    |  ||
Db   223 ----------------GDRGPKGLPGPQG----------LRGPKGDKGFGMPGAPGVKGP- 256

Qy   187 ERDRGAAHSLEPGKENLPGDPTSNATS-RGAEGPLPPPSMPAVAGAAGGLALLLL-----G 241
               :  |   |           ||:  |  || |  |   |
Db   257 -----PGMHGL-PGPVGLPGVGKRGVTGFPGPQGPIGVPGVQGPPG 311

Qy   242 VAGAGGAMCWRRRRRAKPSESRHPG----------------- 257
         :                 |||
Db   312 IPGIG------------KPGQDGIPGQGPGPGKGEGQLPGLPGPGAPGLPGIGKPGFPGPKGD 361

Qy   275 LGLGG-GGGMGPREAEPGELGIALRGGGAAADP--PFCPHYEKVSGDYGHPVYIVQDGP-- 329
         |:||   :|||          |      :|       ||
Db   362 RGMGGVPGALGPR-GEKGPIGAPGIGG---- 425

Qy   330 ------PQSPP 334
            :||
Db   417 GIVGPQGPP 425
```

```
Db   362 RGMGGVPGALGPR-GEKGPIGSPGIGGSSPGEPGLPGIP-------GPMGPPGAIGFPGPKG 414
                                                                   :||
Qy   330 ------PQSPP 334

Db   415 EGGIVGPQGPP 425
```

RESULT 8
US-11-186-284-39
; Sequence 39, Application US2005026493A1
; Publication No. US2005026493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 744
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-39

```
Query Match     5.8%;  Score 142;  DB 7;  Length 744;
Best Local Similarity   23.3%;  Pred. No. 0.00034;
Matches   72;  Conservative  16;  Mismatches  99;  Indels 122;  Gaps  13;

Qy    67 PPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWG 126
         |||||       |  :|     |         | |   |       :   |
Db   198 PPGPHGLPG----------IGKPGGPLPGQPGPK----------------------- 222

Qy   127 HEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPM 186
         :||                  |       |||    |  ||
Db   223 ---------------GDRGPKGLPGPQG----------LRGPKGDKGFGMPGAPGVKGP- 256

Qy   187 ERDRGAAHSLEPGKENLPGDPTSNATS-RGAEGPLPPPSMPAVAGAAGGLALLLL-----G 241
               :  |   |           ||:  |  || |  |   |
Db   257 -----PGMHG--PPGPVGLPGVGKPGVTGFPGPQGPIGKPGAPGEPGRPGPPGP 311

Qy   242 VAGAGGAMCWRRRRRAKPSESRHPG----------------------- 257
         :                 |||
Db   312 IPGIG-----------KPGQDGIPGQGPGPGVGKPGEPGLPGLPGPGPGLPGIGKPGFPGPKGD 361

Qy   275 LGLGG-GGGMGPREAEPGELGIALRGGGAAADP--PFCPHYEKVSGDYGHPVYIVQDGP-- 329
         |:||   :|||          |      :|       ||
Db   362 RGMGGVPGALGPR-GEKGPIGAPGIGG----PPGEPGLPGIPGPMGPPGAIGFPGPKGEG 416

Qy   330 ------PQSPP 334
            :||
Db   417 GIVGPQGPP 425
```

RESULT 9
US-10-821-234-964

; Sequence 964, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
;
; SEQ ID NO 964
; LENGTH: 1166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-964

Query Match   5.8%;   Score 141.5; DB 6;   Length 1166;
Best Local Similarity   28.1%;   Pred. No. 0.00063;
Matches 59;   Conservative 11;   Mismatches 83;   Indels 57;   Gaps 8;

Qy   165 LRVGQSP-----------RGGAVPRKP----------VSEMPMER-------DRGAAHSLEPGK 200
Db   697 LRGGAGPPGPEGKGKAGPGPGPGAACTPGLQCMPGERGGLGSSPGPKGDKG-----EPGG 751

Qy   201 ENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAG-GLALLLGVAGAGGAMCWRRRAKPS 259
Db   752 PGADGVPGKDG-PRGPTGPIGPPGPAGQPGDKGEGGPAPGLPGIAGPRGSPGERGETGPPG 810

Qy   260 ESRHPG-----------PGSFGRGGSLGLGGGGGMGPREAEPGELGIALRGGGAA 303
Db   811 PAGFPGPAPGQNGEPGGPGKGERGAPGEKGEGGGPGVAGPGPGKDGTSGHPGPIG-------- 861

Qy   304 DPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
Db   862 -PPGPRGNRGERGERGSEGSPGHPGQPGPGPP 890

; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-33

Query Match   5.8%;   Score 141.5; DB 7;   Length 1466;
Best Local Similarity   27.6%;   Pred. No. 0.00082;
Matches 61;   Conservative 13;   Mismatches 74;   Indels 73;   Gaps 10;

Qy   171 PRGGAVPRKPVSEMPMERDRGA-----------AHSLEPGKENLPGDPTSNAT------- 218
Db   844 PPGGSGPAGPPGPGQGVKGERGSPGGPGAAGFPGARGLPGPPGSNGNPGPPGPSCSPGKDG 903

Qy   219 PLPP-----------PSMPAVAGAAGGL------------------------------ 256
Db   904 PPGPAGNTGAPGSPGVSGPGKDAGPGEKGSPGAGQGPPGPGAPGPLGIAGITGARGLAGPPG 963

Qy   257 KPSESRHPGP-----GSFGRGGSLGLGG-GGGMGP-------------REAEPGELGIAL 297
Db   964 MPGPRGGSPGPQGVKGEGSGKPGANGLSGERGPPGPGQGLPGLAGTAGEPGRDGNPGSDGLPG 1023

Qy   298 RGG----------GAADPPPFCPHYEKVSGDYGHPVYIVQDGPP 330
Db   1024 RDGSPGGKDGRGENGSPGAP-------------GAPGHP-----GPP 1052

RESULT 10
US-11-186-284-33
; Sequence 33, Application US/11186284
; Publication No. US20050266493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 33
; LENGTH: 1466

RESULT 11
US-10-821-234-1182
; Sequence 1182, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
;
; SEQ ID NO 1182
; LENGTH: 1874
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1182

Query Match   5.6%;   Score 137.5; DB 6;   Length 1874;
Best Local Similarity   25.5%;   Pred. No. 0.0023;
Matches 79;   Conservative 15;   Mismatches 85;   Indels 131;   Gaps 18;

Qy   61   LCPRARPQGPHSSPNYEFYKLIYLVGGAQG-------------RRCEAPPAPNLLLTCDRPDLD 110
Db   602 LTGRPGPVGPPGS---------------GGLKGEPGDVGPGPRGVQGPPGP----AGKP 642

Qy   111 LRFTIKFQEYSPNILWGHEFRSHHDYYIIATSDGTR--------------EGLESLQGGVC 156
Db   643 -------------GRRGR-------AGSDGARGMPGCQTGPRGDRGFDGLIAGLPG-- 676

Qy   157 LTRGMKVLLRVGGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGA 216
Db   677 ------------EKGHRGPDGPSGGPGPGPGDDGERG--DDGEVGPRGLPGEP----GPRGL 719

Qy   217 EGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRAKPSESRHPG-PGSFGRGGSL 275
Db   720 LGPKGPGPGPGPGCVTG-----MDGQPGKGNV-------GPQGEGPGPPGQOGNPGAQ 765

Qy   276 GL-GGGGGMGPREAEPGELGIALRGG--------GAADPPPFCPHYEKVSGDYGHPVYIVQDGP 329
Db   766 GLPGPQGAIGP----PGEKGPLGKPGLPGMPGADGPP------------GHP---GKGP 806

Qy   330 P-----QSPP 334

Db   807 PGEKGGQGPP 816
              ||| | |||

RESULT 12
US-10-821-234-914
; Sequence 914, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Labat, Ivan
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 914
; LENGTH: 1532
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-914

Query Match   5.5%; Score 135.5; DB 6; Length 1532;
Best Local Similarity 23.5%;
Matches   69; Conservative 18; Mismatches 102; Pred. No. 0.0026; Indels 105; Gaps 11;

Qy   65 ARPPGPHSSPSPNYEFYKYLYLVGGAQGRR--------CEAPPAPNLLLTCDRPDLDLRFTKF 117
Db   684 AGEPGPHGPPG-----------------VPGSVGPRKGSSGSPGPQGPPGP----------- 716

Qy   118 QEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVP 177
Db   717 --------------------VGLQGLRGEVGLP-GVK------GDKGPMGP 740

Qy   178 RKPVSEMPEMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLAL 237
Db   741 PGPKGDQGEKGPRGLTG--EPGMRGLPG-AVGEPGAKGAMGPAGPDGHQGPRGPGEQG---- 793

Qy   238 LLLGVAGAGGAMCWRRRRAKPSESRHPG-PGSFGRGGSLGLGGGGMGPREAPGELGIA 296
Db   794 -LTGMPGI------RGPGPGSGDPGKPGLTGPGPQGLPGTPGRPGPGIKGPGAPGKI 843

Qy   297 LRGGGAA--------DPPECPHYEKVSGDYGHPVYIVQDGPPQSP 333
Db   844 VTSEGSSMLTVPGPPGPGPGAMGPPGPGAPGPAGPAGLPGHQEVLNLQGPPGPP 897

RESULT 13
US-10-821-234-1431
; Sequence 1431, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Labat, Ivan
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_SEQ_genes Version 1.0
; SEQ ID NO 1431
; LENGTH: 1366
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1431

Query Match   5.5%; Score 134.5; DB 6; Length 1366;
Best Local Similarity 25.3%;
Matches   89; Conservative 14; Mismatches 114; Pred. No. 0.0027; Indels 135; Gaps 22;

Qy   3 PPHSGPGGV--RVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
Db   321 PGLPGPGIPGPVGAAGATGARGLVGEPGPAGSKGESGNKGEPGSSAG----PQ----- 369

Qy   61 LCPRARPPGPHSSPNYEFYKYLYLVGGAQGRR--------CEAPPAPNLLLTCDRPDLDLRF 113
Db   370 --------GPQGP-------SGEEGKRGPGNGEAGSAGPPGP-------- 395

Qy   114 TIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVG-QSPR 172
Db   396 --------PGLRG-------SPGSR-GLPGADG----------------RAGVMGPP 420

Qy   173 GGAVPRKPVSEMPEMERDRGAAHSLEP--GKENLPGDPTSNATSRGAEGPLPPPSMPAVA 229
Db   421 GSRGASGPAGVRGPNGDAGPRG--EPGLMGPRGLPGSP--GNIGPAGKGEPGV--GLPGID 474

Qy   230 GAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPG-------PGSFGRGGSLGLGGG-G 281
Db   475 RGPG----IGPAGA----------RGEPGNIGFPGKGPTGDPGKNGDKGHAGLAGARG 520

Qy   282 GMGP-----REAPGELGIALRGG-----GAAADPP---FCPHYEKVSGDYGHP 321
Db   521 APGPDGNNGAQGPPGPQGQGV--QCGGKGEQGPAGPPGFQGGLPGPSGPAGEVGKP 570

RESULT 14
US-11-186-284-31
; Sequence 31, Application US/11186284
; Publication No. US20050264493A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MPM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/11/186,284
; CURRENT FILING DATE: 2005-07-21
; PRIOR APPLICATION NUMBER: US/11/186,284
; PRIOR APPLICATION NUMBER: US/10/301,822
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 1366
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-11-186-284-31

Query Match   5.5%; Score 134.5; DB 7; Length 1366;
Best Local Similarity 25.3%;
Matches   89; Conservative 14; Mismatches 114; Pred. No. 0.0027; Indels 135; Gaps 22;

Qy   3 PPHSGPGGV--RVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
Db   321 PGLPGPGIPGPVGAAGATGARGLVGEPGPAGSKGESGNKGEPGSSAG----PQ----- 369

```
Qy   61  LCPRARPPPGPHSSPNYEFYKLYLVGGAQGRR-------CEAPPAPNLLLTCDRPLDLRF  113
Db  370  ------GPPGP---------------------SGEGKGRGPNGEAGSAGPGP--------  395

Qy  114  TIKFQEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVG-QSPR  172
Db  396  -------PGLRG-------SPGSR-GLPGADG-----------------RAGVMGPP  420

Qy  173  GGAVPRKPVSEMPMERDRGAAHSLEP---GKENLPGDPTSNATSRGAEGPLPPPSMPAVA  229
Db  421  GSRGASGPGAGVRGPNGDAGRPG----EPGLMGPRGLPGSP-GNIGPAGKEGPV---GLPGID  474

Qy  230  GAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHPG--------PGSFCRGGSLGLGLGGG-G  281
Db  475  GRGPG-----IGPAGA----------RGEPGNIGFPGPRKGPTGDPGDKGNGDKGHAGLAGARG  520

Qy  282  GMGP-------REAEPGELGIALRGG----GAADPP---FCPHYEKVSGDYGHP  321
Db  521  APGPDGNNGAQGPPGPQGV--QGGKGEQGPAGPPGFQGLPGPSGPAGEVGKP  570
```

```
Query Match             5.4%;
Best Local Similarity   25.8%;
Matches   99;  Conservative   19;  Mismatches  128;  Indels  138;  Gaps   23;
Score 133;  DB 7;  Length 1464;  Pred. No. 0.0039;

Qy    2  GPPHSGPGGVRVGALLLLGVLGVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL  61
Db  848  GPP--GPIG-NVGAPGAKGARG-----SAGP----------PGATGFPGAAAGRVGPP  886

Qy   62  CP--RARPPGPHSSPNYEFYKLYLVGGAQGRRCE-----------APPAPNLLLTCDR  106
Db  887  GPSGNAGPPGPCGPAGKE--------GGKGPRGETGPAGRGEVGPPGPPGP-------  930

Qy  107  PDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATSDGT--REGLESLQGGVCL-----TR  159
Db  931  -------AGEKSPGADGP--------------AGAPGTPGPGPQGGIAGQRGVGLPGQRGER  970
```

```
Qy  160  GMKVLLRVG-------QSPRGGAVPRKPVSEM---------PMERDRGAAHSLE--PGKENLP  204
Db  971  GFPGLPGPSGGEPGPKQGPSGASGERGPPGPMGPPGLAGPGPGESGRREGAPAAEGSPGRDGSP  1030

Qy  205  GDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSESRHP  264
Db  1031 G-----AKGDRGETGPAGPGPCAGPAGPAGPAGPGP-----DRGET  1069

Qy  265  GP-GSFGRGGSLGL-GGGGQGMGPR-------EAEPGELGIALRGG------GAADPPPCPHYE  312
Db  1070 GPAGPAGPVGPVGARGPAGPAGPQGGPRGDKGGETGEQGDRGIKGHRGFSGLQGPGPGPGSPGEQ  1129

Qy  313  KVSGDYGHPVYIVQDGP--PQSPP  334
Db  1130 GPSG---------ASGPAGPRGPP  1144
```

Search completed: December 21, 2005, 14:55:34
Job time : 11.5849 secs

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```
OM protein - protein search, using sw model

                    GenCore version 5.1.6
                    Copyright (c) 1993 - 2005 Compugen Ltd.

Run on:             December 21, 2005, 14:22:09 ; Search time 28.044 Seconds
                                                   (without alignments)
                                                   1561.068 Million cell updates/sec

Title:              US-10-021-121-2
Perfect score:      2450
Sequence:           1 MGPPHSGPGGVRVGALILLG.........TTLLRQRASVEAEACQHGPL 455

Scoring table:      BLOSUM62
                    Gapop 10.0 , Gapext 0.5

Searched:           283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:     283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing:    Minimum Match 0%
                    Maximum Match 100%
                    Listing first 45 summaries

Database :          PIR_80:*
                    1: pir1:*
                    2: pir2:*
                    3: pir3:*
                    4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
```

```
                              SUMMARIES

Result         %
No.    Score   Query  Match  Length  DB  ID        Description
----   -----   -----  -----  ------  --  --        -----------
 1     628.5   25.7   336    346     2   I49766     hepatoma transmemb
 2     623     25.4   346    346     2   S46993     elk ligand - human
 3     620.5   25.3   333    333     2   I84743     hepatoma transmemb
 4     604.5   24.7   345    345     2   I48780     Stra1/Eplg2 protei
 5     599.5   24.5   345    345     2   I58406     LERK-2 - rat
 6     214.5   8.8    237    237     2   T19914     hypothetical prote
 7     179     7.3    238    238     2   I38849     LERK-3 - human
 8     176     7.2    209    209     2   A54984     ELF-1 protein prec
 9     175.5   7.2    213    213     2   JE0322     ephrin-A2 - human
10     170.5   7.0    228    228     2   A57004     repulsive axon gui
11     169.5   6.9    201    201     2   I38850     LERK-4 - human
12     167.5   6.8    228    228     2   I58170     LERK-7 precursor -
13     166     6.8    205    205     2   A36377     B61 protein precur
14     159     6.5    680    680     1   S31116     collagen alpha 1(X
15     154.5   6.3    1049   1049    1   CGBO7S     collagen alpha 1(I
16     153.5   6.3    1670   1670    1   CGHU3B     collagen alpha 3(I
17     151.5   6.2    301    301     2   B31219     collagen 2 - Caeno
18     149     6.1    325    325     2   T32248     hypothetical prote
19     149     6.1    569    569     2   S42886     collagen - silkwor
20     148.5   6.1    316    316     2   T20497     hypothetical prote
21     148     6.0    921    921     1   S42617     collagen alpha 1(I
22     146.5   6.0    1315   1315    1   A56101     collagen alpha 1(X
23     146.5   6.0    1492   1492    1   A40333     collagen alpha 1,'(
24     146.5   6.0    1774   1774    1   B56101     collagen alpha 1(X
25     146     6.0    675    675     2   S20819     collagen alpha 3(I
26     146     5.9    305    305     2   T20006     hypothetical prote
27     145     5.9    674    674     2   S13301     collagen alpha 1(I
28     145     5.9    931    931     1   S13580     collagen alpha 1(I
29     144.5   5.9    438    438     2   S53787     collagen alpha cha
30     144     5.9    1027   1027    2   S28774     collagen alpha cha
31     143     5.9    1747   1747    2   A54121     collagen alpha-4 c
32     142.5   5.8    635    635     2   A57131     collagen alpha 2(V
33     142.5   5.8    743    743     2   S23779     collagen alpha 2(V
34     142.5   5.8    1496   1496    1   CGHU2V     collagen alpha 2(V
35     142     5.8    614    614     2   T33149     hypothetical prote
36     142     5.8    744    744     2   S15435     collagen alpha 1(V
37     142     5.8    1029   1029    2   S21369     collagen alpha 2(I
38     142     5.8    1763   1763    2   S16366     collagen alpha 2(I
39     141.5   5.8    319    319     2   CGHU7L     collagen alpha 1(I
40     141     5.8    744    744     1   T32250     hypothetical prote
41     141     5.8    744    744     1   A34246     collagen alpha 1(V
42     141     5.8    744    744     1   S23298     collagen alpha 1(V
43     140.5   5.7    305    305     2   T30165     hypothetical prote
44     140     5.7    304    304     2   T22482     hypothetical prote
45     140     5.7    680    680     1   CGHU1D     collagen alpha 1(X
```

```
                              ALIGNMENTS

RESULT 1
I49766
hepatoma transmembrane kinase ligand - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
A;accession: I49766
R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews,
Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995
A;Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine kin
A;Reference number: I49766; MUID:95199254; PMID:7534404
A;Accession: I49766
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-336 <RES>
A;Cross-references: UNIPROT:P52800; UNIPARC:UPI0000020B55; GB:L38847; NID:g769677; PIDN:
A;Genetics:
A;Gene: HTK

Query Match        25.7%;  Score 628.5;  DB 2;  Length 336;
Best Local Similarity  41.8%;  Pred. No. 3.2e-37;
Matches 137;  Conservative 49;  Mismatches 129;  Indels 13;  Gaps 5;

Qy     14  GALLLLGVLGLVSGLSLEPYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPGPHSS  73
               |:|   |||||||||||  :||:|||| ||||| |:||||||:|:||||||||
Db     17  GLIMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV  73

Qy     74  PNYEFYKLYLVGGAQCRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH  133
               |:|||  |||| ||  | ||:  |::  ||||| |||:||||||:|:||:|||| | |||
Db     74  GQYEYYKVYMVDKDQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK  133

Qy    134  DYYIIATSDGTREGLESLQGGVCLTRGMKYLLRVGQ--SPRGGAVPRKPVSEMPMER-DR  190
               |||||||||||||  ||  ||:|:   |:||||||:||:|    |  | :|::||| :|
Db    134  DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN  193

Qy    191  GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC  250
               |||::|||||||||||||||||||||:||||  ||||||||:|||  ||:|::|:|:::|:
Db    194  GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL  253

Qy    251  WRRRRAKPSESRHPGPGSFGRGGSLGLGGGGMGPREAEPGELGTALRGGGAADPPFCPH  310
               :|: ||:| : :||  |: |:|:  :  |:  | |:  || | |||::||      |||
Db    254  KYRRRHRKHSPQHTTTLSLSTIATPKRGGNN---NGSEPSDVIIPLR---TADSVFCPH  306

Qy    311  YBKVSGDYGHPVYIVYIVQDGGPPQSPPNIYY  338
               |||||||||||||||   |||||:| ||| |||
Db    307  YBKVSGDYGHPVYIVQEMPQSPANIYY  334

RESULT 2
S46993
elk ligand - human
C;Species: Homo sapiens (man)
C;Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
```

```
C;Accession: S46993
R;Beckmann, M.P.; Cerretti, D.P.; Baum, P.; vanden Bos, T.; James, L.; Farrah, T.; Kozlo
  EMBO J. 13, 3757-3762, 1994
A;Reference number: S46993
A;Title: Molecular characterization of a family of ligands for eph-related tyrosine kina
A;Accession: S46993
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-346 <BEC>
A;Cross-references: UNIPROT:P98172; UNIPARC:UPI000006222D; GB:U09304; NID:g538366; PIDN:

Qy      Query Match      25.4%;   Score 623;   DB 2;   Length 346;
        Best Local Similarity   39.2%;   Pred. No. 8e-37;
        Matches 143;   Conservative 48;   Mismatches 116;   Indels 58;   Gaps 9;

Qy    8  PGGVRVGALLLLGVLGLVSGL---------SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL    61
Db    4  PGQRWLGKWLVAMVWWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII     63

Qy   62  CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS   121
Db   64  CPRAEAGRP-------YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS  118

Qy  122  PNLWGHEFRSHDYYIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV    181
Db  119  PNYMGLEFKXHHDYYITSTSNGSLEGLENREGGVCVRTRTMKIIMKVGQDPNAVTPEQLTT  178

Qy  182  SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---   236
Db  179  SRPSKEADNTVKNATQAPEGSRGSLGDSDGKHETVNQEEKSGP------             231

Qy  237  -----LLLLGVAGAGGA--------MCWRRRAKPSESRHPGPGSFGRGGGSLGL        277
Db  232  GFPNSKVALFAAVGAGCVIFLLIIIFLTVLLLKRKIRKHTQQ-----RAAALSL        282

Qy  278  ---GGGGGMGPREAEPGELGIALRGGGGAAADPPFCPHYEKVSGDYGHPVIYIVQDGPPQSP  333
Db  283  STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVIVIQEMPPQSP    339

Qy  334  PNIIY  338
Db  340  ANIYY  344


RESULT 3
I84743
hepatoma transmembrane kinase ligand - human
C;Species: Homo sapiens (man)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 09-Jul-2004
C;Accession: I84743
R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews
  Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995
A;Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine kin
A;Reference number: I49766; MUID:95199254; PMID:7534404
A;Accession: I84743
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-333 <RES>
A;Cross-references: UNIPROT:P52799; UNIPARC:UPI00000129C9B; GB:L38734; NID:g769675; PIDN:

Qy      Query Match      25.3%;   Score 620.5;   DB 2;   Length 333;
        Best Local Similarity   40.5%;   Pred. No. 1.1e-36;
        Matches 133;   Conservative 52;   Mismatches 130;   Indels 13;   Gaps 5;

Qy   14  GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS   73
Db   14  GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGGLVLYPIGDKLDIICPKV---DSKTV    70

Qy   74  PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH  133
```

```
Db   71  GQYEYKVXVMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQRKNK            130
Db  134  DYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQ---SPRGGAVPRKPVSEMPMER-DR  190
Db  131  DYYITSTSNGSLEGLDNQEGGVCVQTRAMKILMKVGQDASSAGSTRNKDFTRRPELEAGTN  190
Qy  191  GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVLGLVSGL   250
Db  191  GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIILVLLL    250
Qy  251  WRRRRAKPSESRHPGPGSFGRGGGSLGLGGGGGMGPREAEPGELGIALRGGGGAADPPFCPH  310
Db  251  KYRRHRHRKHSPQHTTTLSLSTLATPKRSGNN---NGSEPSDIIIPLR---TADSVFCPH  303
Qy  311  YEKVSGDYGHPVIYIVQDGPPQSPPNIIY  338
Db  304  YEKVSGDYGHPVIVIQEMPPQSPANIYY   331


RESULT 4
I48780
Stra1/Eplg2 protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I48780; A55507; A55062; S52670
R;Bouillet, P.; Oulad-Abdelghani, M.; Vicaire, S.; Garnier, J.M.; Schubaur, B.; Dolle, F
  Dev. Biol. 170, 420-433, 1995
A;Title: Efficient cloning of cDNAs of retinoic acid-responsive genes in P19 embryonal ce
A;Reference number: I48780; MUID:95377533; PMID:7649373
A;Accession: I48780
A;Molecule type: mRNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-345 <RES>
A;Cross-references: UNIPROT:P52795; UNIPARC:UPI00000018AC; EMBL:Z48781; NID:g747858; PID
R;Fletcher, F.A.; Renshaw, B.; Hollingsworth, T.; Baum, P.; Lyman, S.D.; Jenkins, N.A.; C
  Genomics 24, 127-132, 1994
A;Title: Genomic organization and chromosomal localization of mouse Eplg2, a gene encodi
A;Reference number: A55507; MUID:95203867; PMID:7896266
A;Accession: A55507
A;Molecule type: DNA
A;Status: preliminary
A;Residues: 1-345 <FLE>
A;Cross-references: UNIPARC:UPI000000018AC; GB:U07598
R;Shao, H.; Lou, L.; Pandey, A.; Pasquale, E.B.; Dixit, V.M.
  J. Biol. Chem. 269, 26606-26609, 1994
A;Title: cDNA cloning and characterization of a ligand for the Cek5 receptor protein-tyro
A;Reference number: A55062; MUID:95014510; PMID:7923389
A;Accession: A55062
A;Molecule type: mRNA
A;Status: preliminary; not compared with conceptual translation
A;Residues: 1-89, 'T', 91-345 <SHA>
A;Cross-references: UNIPROT:UPI00000016CADF; GB:U12983; NID:g575928; PIDN:AAA53231.1; PID:g
A;Gene: EPLG2
A;Genetics:

Qy      Query Match      24.2%;   Score 604.5;   DB 2;   Length 345;
        Best Local Similarity   37.9%;   Pred. No. 1.6e-35;
        Matches 136;   Conservative 51;   Mismatches 107;   Indels 65;   Gaps 10;

Qy   15  ALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHS   72
Db   15  AMVVLTLCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP--   72

Qy   73  SPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSH  132
Db   73  ---YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPHQEIRFTIKFQEFSPNYMGLEFKXY  129

Qy  133  HDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGA  192
Db  130  HDYYITSTSNGSLEGLENREGGVCVRTRTMKIIVMKVGQDD-NAVTPEQLTTSRPSKESDNT  188

Qy  193  AHSLEPGKENLPGDPTSNATSRGAEGP--------LPPPSMPAVAGAAGG-----LA   236
```

```
Db  189  VKT------------ATQAPGRGSQGDSDGKHETVNQEEKSGPGAGGGGSGSGDSDSFFNSK  236
Qy  237  LILLLGVAGAGGA------MCWRRRAKPSESRHPGPGSFGRGGSLGL----GG  279
Db  237  VALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ------RAAALSLSTLLASP  287
Qy  280  GGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY  338
Db  288  KGDSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVVIVQEMPPQSPANIYY  343
```

RESULT 5
I58406
LERK-2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: I58406
R;Fletcher, F.A.; Carpenter, M.; Shilling, H.; Baum, P.; Ziegler, S.; Gimpel, S.; Hollin...
Oncogene 9, 3241-3248, 1994
A;Title: LERK-2, a ligand for the receptor tyrosine kinase ELK, is evolutionarily conse...
A;Reference number: I58406; MUID:95022634; PMID:7936648
A;Accession: I58406
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-345 <RES>
A;Cross-references: UNIPROT:P52796; UNIPARC:UPI0000129C98; EMBL:U07560; NID:g563118; PID

Query Match 24.5%; Score 599.5; DB 2; Length 345;
Best Local Similarity 37.6%;
Matches 135; Conservative 52; Mismatches 107; Indels 65; Gaps 10;

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Qy   15  ALILLGVLGLVSGL--SLEPVYVNNSANKRFQOAEGGYVLYPQIGDRLDLLCPRARPPGPHS  72
Db   15  AMVLTLCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRABAGRP--  72
Qy   73  SPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSH  132
Db   73  ---YEYYKLYLVRPEQAAACSTVLDPNVLVTCNKPQOEIRFTIKFQEESPNYMGLEFKKY  129
Qy  133  HDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKEVSEMPMERDRGA  192
Db  130  HDYYITSTSNGSLEGLENRBGGVCRITMKIVMKVGQDP-NAVTPEQLTISRPSKESDNT  188
Qy  193  AHSLEPGKENLPGDPTSNATSRGAEGP-------LPPPSMPAVAGNAAGG------LA  236
Db  189  VKT------------ATQAPGRGSQGDSDGKHETVNQEEKSGPGAGGGGSGSGDTDSFFNSK  236
Qy  237  LILLGVAGAGGA------MCWRRRAKPSESRHPGPGSFGRGGSLGL----GG  279
Db  237  VALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHKTQQ------RAAALSLSTLLASP  287
Qy  280  GGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY  338
Db  288  KGDSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVVIVQEMPPQSPANIYY  343
```

A;Experimental source: clone C43F9
C;Genetic:
A;Gene: CESP:C43F9.8
A;Map position: 4
A;Introns: 32/2; 96/3; 214/1

RESULT 6
T19914
hypothetical protein C43F9.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19914
R;Morimore, B.,
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19195
A;Accession: T19914
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-237 <WIL>
A;Cross-references: UNIPROT:Q9U3M2; UNIPARC:UPI000007B016; EMBL:Z82262; PIDN:CAB54195.1;

Query Match 8.8%; Score 214.5; DB 2; Length 237;
Best Local Similarity 25.7%; Pred. No. 4e-08;
Matches 53; Conservative 41; Mismatches 83; Indels 29; Gaps 6;

```
Qy   11  VRVGALLLLGVLGLVS-GLSLEPVYVNNSANKRFQAEG-GYVLYPQIGDRLDLLCPRARPP  68
Db    1  MQIATFILLSLPFFIGWARKIPDIWWISSNPIFDVSNTDHVISVHIGDRVSIRCPKSDET  60
Qy   69  GPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLLRFTIKFQEYSPNLWGHE  128
Db   61  G-----KYEYSYIYMVSDEEYDHCFL-SKPRLVGACDNQTINASINIVFRSFTPTPGGFE  114
Qy  129  FRSHHDYYIIA---------TSDGTREGLESLQGGVCLTRGMKVLLRVG  169
Db  115  FQPGKNYFLISKSEVDALIIYETANQIFPGTSDGTLEGIDRKKDGLICTAKQMKIKFEVGQ  174
Qy  170  SPRGGAVPRKPVSEMPMERDRGAAHS  195
Db  175  DRRGIENPK--FAARTLKKDRDAEHS  198
```

RESULT 7
I38849
LERK-3 - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I38849
R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.; Lyman, S.D.; ...
Oncogene 10, 299-306, 1995
A;Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs encod...
A;Reference number: I38849; MUID:95140419; PMID:7838529
A;Accession: I38849
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-238 <RES>
A;Cross-references: UNIPROT:P52797; UNIPARC:UPI000129C8F; EMBL:U14187; NID:g642832; PIDN
C;Genetics:
C;Gene: EPLG3
A;Cross-references: GDB:438336; OMIM:601381
A;Map position: 1q21-1q22
A;Cross-references: GDB:438336; OMIM:601381
C;Superfamily: axon guidance signal protein

Query Match 7.3%; Score 179; DB 2; Length 238;
Best Local Similarity 28.4%; Pred. No. 1.3e-05;
Matches 65; Conservative 24; Mismatches 80; Indels 60; Gaps 12;

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Qy    7  GPGGVRVGALLLLGVILGLVSGLSLEPVYVNNSANKRFQAEGGYVLYPQIGDRLDLLCP-R  64
Db   24  GPG---------GALG-----NRHAVYMNNSSNQHLRRE-GYTVQVNVANDYLDIYCPHYN  67
Qy   65  ARPPGPHSSP----NYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL--DLRFTIKF  117
Db   68  SSGVGPGAGPGPGGGGAEQYVLYMVSRNGYRTCNASQGFK-RWECNRPHAPHSPIKFSEKF  126
Qy  118  QEYSPNLWGHEFRSHHDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVP  177
Db  127  QRYSAFSLGTEFHAGHEYYYISTPTHNLH------WKCLR--MKVFVCCASTSHSG---  174
Qy  178  RKPVSEMP--------MERDGAAHSLE------PGKENLP  204
Db  175  EKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP  223
```

RESULT 8
A54984
ELF-1 protein precursor - mouse
N;Alternate names: Cek7 ligand

C;Species: Mus musculus (house mouse)
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 09-Jul-2004
C;Accession: A54984; A55873
R;Cheng, H.J.; Flanagan, J.G.
Cell 79, 157-168, 1994
A;Title: Identification and cloning of ELF-1, a developmentally expressed ligand for the
A;Reference number: A54984
A;Accession: A54984; MUID:95007776; PMID:7522971
A;Status: preliminary
A;Accession: A54984
A;Molecule type: mRNA
A;Residues: 1-209 <CHE>
A;Cross-references: UNIPROT:P52801; UNIPARC:UPI000000020CE3; GB:U14941; NID:g558836; PIDN:
J. Biol. Chem. 270, 3467-3470, 1995
A;Title: cDNA cloning and characterization of a Cek7 receptor protein-tyrosine kinase li
R;Shao, H.; Lou, L.; Pandey, A.; Verderame, M.F.; Siever, D.A.; Dixit, V.M.
A;Reference number: A55873
A;Accession: A55873; MUID:95181289; PMID:7876076
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-209 <SHA>
A;Cross-references: UNIPARC:UPI000000020CE3; GB:U14752; NID:g681886; PIDN:AAA68520.1; PID
C;Superfamily: axon guidance signal protein
C;Keywords: lipoprotein; membrane protein

```
Qy   33  VYWNSANKRFQAE------GGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA   87
             ||||          : ||||||||| | ||||||    |||||| |||  |:
Db   35  VYWNRSNPRFQVSAVGDGGGYTVEVSINDYLDIYCPHYGAPLP--PAERMERYILYMVNGE   93

Qy   88  QGRRCEAPPAPNLLLTCDRPDL--DLRFTIKFQEYSPNLWGHEFRSHHDYIIATSDGT    144
             |  |||      | ||     | |   |:
Db   94  GHASCDHRORGFKRWECNRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYISATP--   151

Qy  145  REGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLP   204
             |
Db  152  -----PNLVDRPCLR--LKVYVR----------------------PTNETLY          174

Qy  205  GDP------TSNATSRGAEG   218
             :|:
Db  175  EAPEPIFTSNSSCSGLGG     192
```

RESULT 9
JE0322
ephrin-A2 - human
C;Species: Homo sapiens (man)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
C;Accession: JE0322
R;Pedeutour, F.; Grosgeorge, J.; Logtenberg, T.
R;Aasheim, H.; Pedeutour, F.; Grosgeorge, J.; Logtenberg, T.
A;Title: Cloning, chromosal mapping, and tissue expression of the gene encoding the huma
Biochem. Biophys. Res. Commun. 252, 378-382, 1998
A;Reference number: JE0322; MUID:99045414; PMID:9826538
A;Accession: JE0322
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-213 <AAS>
A;Cross-references: UNIPROT:O43921; UNIPARC:UPI000016A442; GB:AJ007292; NID:g3688367; PI
C;Superfamily: axon guidance signal protein

Query Match   7.2%; Score 175.5; DB 2; Length 213;
Best Local Similarity 36.8%; Pred. No. 2e-05;
Matches 43; Conservative 14; Mismatches 51; Indels 9; Gaps 3;

```
Qy   33  VYWNSANKRFQA-----EGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA   87
             ||||          |||||||| | ||||| |||||||  || |||  |:
Db   39  VYWNRSNPRFHAGAGDDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMEHYVLYMVNGE   97

Qy   88  QGHASCDHRORGFKRWECNRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYISAT     154
             |:|: |        |:|||
Db   98  GHASCDHRORGFKRWECNRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYIIATS     141
```

RESULT 10
A57084
repulsive axon guidance signal protein RAGS precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: A57084
R;Drescher, U.; Kremoser, C.; Handweker, C.; Loeschinger, J.; Noda, M.; Bonhoeffer, F.
Cell 82, 359-370, 1995
A;Title: In vitro guidance of retinal ganglion cell axons by RAGS, a 25 kDa tectal prote
A;Reference number: A57084; MUID:95360980; PMID:7634326
A;Accession: A57084
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-228 <DRE>
A;Cross-references: UNIPROT:P52804; UNIPARC:UPI000129C92; GB:X90377; NID:g1061113; PIDN:
C;Superfamily: axon guidance signal protein
C;Keywords: glycoprotein; membrane protein; phosphatidylinositol linkage
F;1-20/Domain: signal sequence #status predicted <SIG>

Query Match   7.0%; Score 170.5; DB 2; Length 228;
Best Local Similarity 28.9%; Pred. No. 5e-05;
Matches 73; Conservative 30; Mismatches 91; Indels 59; Gaps 13;

```
Qy   16  LLLLGVLGL-VSGLSLEP----------VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPR   64
             :|| |   |:.|| |              |||||   ||||  | |||
Db    6  MLLLAVAALWVCVRGQEPGRKAVADRYAVYWNSTNPRFQ-QGDVHIDVCINDLDVFCPH   64

Qy   65  ARPPGPHSSPNYEFYKLYLVG------------GAQGRRCEAPPAPNLLLTCDRPDLDLR  112
             |       ||||  |:|
Db   65  YEDSVPEDKT--ERYVLYMVNFDGYSSCDHISKGFKRWECNRPHSPN-----------   113

Qy  113  FTIKFQEYSPNLWGHEFRSHHDYYIIATS--DGTREGLESLQGGVCLTRGMKVLLRVGQ   169
             |:||||   || ||| | || || | |            |  |:|
Db  114  FSEKFQLFTPFSLGFEFRPGREYFYISSAIPDNGRRS--------CLK--LKVFVR---  159

Qy  170  SPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGABGPLPPPSMP--A  227
             |          |      :|||
Db  160  -PANSCMKTIGVHDRVFDVNDKVENSLEPADDTV--RBSAEPSRG-ENAAQTRIPIRL   214

Qy  228  VAGAAGGLALLLL   240
             | |||::|||:|:
Db  215  LATLLFLLAMLLI   227
```

RESULT 11
I38850
LERK-4 - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I38850
R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.; Lyman, S.D.;
Oncogene 10, 299-306, 1995
A;Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs encodi
A;Reference number: I38849; MUID:95140419; PMID:7838529
A;Accession: I38850
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-201 <RES>
A;Cross-references: UNIPROT:P52798; UNIPARC:UPI000129C90; EMBL:U14188; NID:g642834; PIDN
A;Gene: GDB:EPLG4
A;Cross-references: GDB:438337; OMIM:601380
A;Map position: 1q21-1q22
A;Genetics:
C;Superfamily: axon guidance signal protein

Query Match   6.9%; Score 169.5; DB 2; Length 201;
Best Local Similarity 29.9%; Pred. No. 5.1e-05;
Matches 66; Conservative 18; Mismatches 82; Indels 55; Gaps 10;

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Qy   24  LVSGLSL-EPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLY   82
             |||       |||
```

```
Db   20  LRGGSSLRHVYVWNSSNPRL-LRGDAVVELGLNDYLDIVCPHYEGPGPPEGP--ETFALY  76
Db   83  LVGGAQGRRCEAP-PAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIATS  141
Db   77  MVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGPEFLPGETTYYISVP  136
Db  142  DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPERDRGAAHSLEPGKE  201
Db  137  --TPE-----SSGQCL------------------RLQVSVCCKERKSESAHPV------  164
Qy  202  NLPGDPTSNATS--RGAEGPLPPPSMPAVAGAAGGLALLLLL  240
Db  165  --GSPGESGTSGWRGGGDTPSP-------------LCLLLL  189
```

RESULT 12
I58170
LERK-7 precursor - human
N;Alternate names: AL-1
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I58170; G01812
R;Kozlosky, C.J.; VandenBos, T.; Park, L.S.; Cerretti, D.P.; Carpenter, M.K.
submitted to the EMBL Data library, May 1995
R;Reference number: G08477
R;Winslow, J.W.; Moran, P.; Valverde, J.; Shih, A.; Yuan, J.Q.; Wong, S.C.; Tsai, S.P.;
Neuron 14, 973-981, 1995
A;Title: Cloning of AL-1, a ligand for an Eph-related tyrosine kinase receptor involved
A;Reference number: I58170; MUID:95267434; PMID:7748564
A;Accession: I58170
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-228 <RES>
A;Cross-references: UNIPROT:P52803; UNIPARC:UPI000000129C93; GB:S77167; NID:g914184; PID:g...
A;Cross-references: UNIPARC:UPI0000129C93; EMBL:U26403; NID:g1019430; PIDN:AAB60377.1; P
A;Map position: 13q33-13q33
A;Superfamily: axon guidance signal protein

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Query Match           6.8%; Score 167.5; DB 2; Length 228;
Best Local Similarity 28.8%; Pred. No. 8.1e-05;
Matches  65; Conservative  29; Mismatches  81; Indels  51; Gaps  11;

Qy   33  VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVG------  85
Db   34  VYWNSSNPFQ-RGDYHIDVCINDYLDVFCPHYEDSVEEDKT--ERYVLYMVNFDGYSAC  90
Qy   86  -----GAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYIIAT  140
Db   91  DHTSKGFKRWECNRPHSPN------GPLKFSEKFQLFTPFSLGFEFRPRGREYFYISS  141
Qy  141  S---DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPERDRGAAHSLE  197
Db  142  AIPDNGRRS------------CLK-LKVFVR----PTNSCMKTIGVHDRVPDVNDKVENSLE  186
Qy  198  PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLLGVA  243
Db  187  PADDTV---HESAEPSRG-ENAAQTPRIPSRL-------LAILLFLLA  223
```

RESULT 13
A36377
B61 protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004
C;Accession: A36377
R;Holzman, L.B.; Marks, R.M.; Dixit, V.M.

Mol. Cell. Biol. 10, 5830-5838, 1990
A;Title: A novel immediate-early response gene of endothelium is induced by cytokines and
A;Reference number: A36377; MUID:91042512; PMID:2233719
A;Accession: A36377
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-205 <HOL>
A;Cross-references: UNIPROT:P20827; UNIPARC:UPI00001299C89; GB:M57730; GB:M57476; NID:g17...
C;Superfamily: axon guidance signal protein

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Query Match           6.8%; Score 166; DB 2; Length 205;
Best Local Similarity 27.5%; Pred. No. 9.2e-05;
Matches  46; Conservative  31; Mismatches  74; Indels  16; Gaps  5;

Qy   18  LLGVLGLVSGSLSLEPYVWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPN--  75
Db    8  LLGLCCSLAAADRHTVFWNSSNPKFRNE-DYTIHVQLNDYVDIICPHYE---DHSVADAA  63
Qy   76  YEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSH  132
Db   64  MEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFTPFTLGKFKEG  123
Qy  133  HDYYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRK  179
Db  124  HSYYISKPIHQHEDR------CLRLKVTVSGKITHSPQAHVNPQB  163
```

RESULT 14
S31216
collagen alpha 1(X) chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: S31216; S28807; S22215; S30127; I48299; S26397; S31830
R;Kong, R.Y.C.; Kwan, K.M.; Lau, E.T.; Thomas, J.T.; Boot-Handford, R.P.; Grant, M.E.; Ch
Eur. J. Biochem. 213, 99-111, 1993
A;Title: Intron-exon structure, alternative use of promoter and expression of the mouse c
A;Reference number: S31216; MUID:93238750; PMID:8477738
A;Accession: S31216
A;Molecule type: DNA
A;Residues: 1-680 <KON>
A;Cross-references: UNIPROT:O05306; UNIPARC:UPI00001GCBAA; EMBL:221610; NID:g49793; PIDN
R;Elima, K.; Eerola, I.; Rosati, R.; Metsaeranta, M.; Garofalo, S.; Peraelae, M.; de Cron
Biochem. J. 289, 247-253, 1993
A;Title: The mouse collagen X gene: complete nucleotide sequence, exon structure and exp
A;Reference number: S28807; MUID:93143676; PMID:8424763
A;Accession: S28807
A;Molecule type: DNA
A;Residues: 1-285, 'A',287-680 <ELI>
A;Cross-references: UNIPROT:UPI000026913; EMBL:X67348; NID:g50480; PIDN:CAA47763.1; PID
R;Elima, K.; Metsaeranta, M.; Kallio, J.; Peraelae, M.; Eerola, I.; Garofalo, S.; de Cron
Biochim. Biophys. Acta 1130, 78-80, 1992
A;Title: Specific hybridization probes for mouse alpha-2(IX) and alpha-1(X) collagen mRN
A;Reference number: S22215; MUID:92182017; PMID:1543751
A;Accession: S22215
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 385-450, 'K',452-627 <ELA>
A;Cross-references: UNIPROT:UPI00001GCBAB; EMBL:X63013; NID:g49795; PIDN:CAA44741.1; PID
R;Apte, S.S.; Olsen, B.R.
Matrix 13, 165-179, 1993
A;Title: Characterization of the mouse type X collagen gene.
A;Reference number: S30127; MUID:93261248; PMID:8492743
A;Accession: S30127
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12, 'F',14-26, 'S',28-247, 'L',249-285, 'A',287-305, 'F',307-416, 'S',418-499,'L'
A;Cross-references: UNIPARC:UPI00001773E5
R;Apte, S.; Seldin, M.F.; Hayashi, M.; Olsen, B.R.
Eur. J. Biochem. 206, 217-224, 1992
A;Title: Cloning of the human and mouse type X collagen genes and mapping of the mouse ty
A;Reference number: I48299; MUID:92267014; PMID:1587271
A;Accession: I48299
A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA
A;Residues: 52-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'L',501-566,'C',568,'
A;Cross-references: UNIPARC:UPI000016CCAC; EMBL:X65121; NID:g50482; PIDN:CAA46237.1; PID
J. Biol. Chem. 263, 581-587, 1988
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-680/Domain: collagen alpha 1(X) chain #status predicted <MAT>
F;553-679/Domain: complement C1q carboxyl-terminal homology

Qy   1 MGPPHSGPGGV-RVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLD 59
         ||||| ||| | : | ||||||||||||||||::| | :| ::
Db   1 IGPP--GPSGVGRRGENGPPGQPGI-------------------KGDRGPGEMG----- 244

Qy   60 LLCPRAPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQE 119
         |||| | | : | | : |: |||:| ||:|:|| | | | ||
Db 245 ----PSGPPGQGPP-----------GKQGR--EGIGKPGAIGSPGQPGI-------- 277

Qy 120 YSPNLWGHEFRSHHDYYIIATSDGT------REGLESLQGGVCLTRGMKVLLRVGQSPRGGA 175
         : :| || | | | |:| | | | ::|| :|| |
Db 278 --PGEKGHPGSPG------------IAGPPGAPGEGKQGLPGLRG----ORG-- 314

Qy 176 VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPSMPAVAGAGL 235
         :||| : | ||: ||: ::| | | ||| |
Db 315 LPGAPGA-----KGERGPAG---HPGEPGLPGSP------GNMGPQGPKGIPGNHGIPGAKGEI 364

Qy 236 ALILLGVAGAGGAMCWRRRRAKP--------SESRHPG--------------PGSFGRGGSILGLGGGGG 282
         ||| |:| |||| || | | || | || :: |: ||
Db 365 G--LVGPAGPPGA----RGARGPPGLDGKTGYPGPPGLNGPKGNPGLPGQKGDPGVGGTPG 419

Qy 283 M--------------GPREAEPGELGLALRGGGAADPPFCPHYEKVSGDYGHPVY 323
                        || | | | | | | | | |
Db 420 LRGPVGPVGAKGVPGHNGEAGPR-GEPGIPGTR----GPTGPPGVPGFPGSKGDPGNP-- 472

Qy 324 IVODGP---------PQSPP 334
          |:| | | |
Db 473 -GAPGPAGIATKGLNGPTGPP 492

RESULT 15
CGB07S
collagen alpha 1(III) chain - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 04-Dec-1986 #sequence revision 04-Dec-1986 #text change 09-Jul-2004
C;Accession: A02862; A38001; A38002; A38003; A38004; A38005; S71946
R;Fietzek, P.P.; Allmann, H.; Rauterberg, J.; Henkel, W.; Wachter, E.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 809-820, 1979
A;Title: The covalent structure of calf skin type III collagen. I. The amino acid sequen
A;Reference number: A02862; MUID:80026026; PMID:488906

Query Match   6.5%; Score 159; DB 2; Length 680;
Best Local Similarity   25.5%;
Matches 97; Conservative 30; Mismatches 108; Indels 146; Gaps 24;

A;Molecule type: protein
A;Residues: 243-422 <DEW1>
A;Cross-references: UNIPARC:UPI000173B8B
R;Bentz, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 833-840, 1979
A;Title: The covalent structure of calf skin type III collagen. III. The amino acid seque
A;Accession: A38002

A;Molecule type: protein
A;Residues: 423-571 <BEN>
A;Cross-references: UNIPARC:UPI000173B8C
R;Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 841-850, 1979
A;Title: The covalent structure of calf skin type III collagen. IV. The amino acid sequen
A;Reference number: A38003; MUID:80026029; PMID:488909

A;Molecule type: protein
A;Residues: 572-808 <LAN>
A;Cross-references: UNIPARC:UPI000173B8D
R;Dewes, H.; Fietzek, P.P.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 851-860, 1979
A;Title: The covalent structure of calf skin type III collagen. V. The amino acid sequen
A;Reference number: A38004; MUID:80026030; PMID:488910

A;Molecule type: protein
A;Residues: 809-947 <DEW2>
A;Cross-references: UNIPARC:UPI000173B8E
R;Allmann, H.; Fietzek, P.P.; Glanville, R.W.; Kuehn, K.
Hoppe-Seyler's Z. Physiol. Chem. 360, 861-868, 1979
A;Title: The covalent structure of calf skin type III collagen. VI. The amino acid sequen
A;Accession: A38005; MUID:80026031; PMID:488911

A;Molecule type: protein
A;Residues: 948-1049 <ALL>
A;Cross-references: UNIPARC:UPI000173B8F
A;Experimental source: skin
R;Henkel, W.
Biochem. J. 318, 497-503, 1996
A;Title: Cross-link analysis of the C-telopeptide domain from type III collagen.
A;Reference number: S71946; MUID:96404897; PMID:8809038
A;Accession: S71946

A;Molecule type: protein
A;Residues: 87-106;1017-1029;1037-1049 <HEN>
A;Cross-references: UNIPARC:UPI000173B90; UNIPARC:UPI000173B91; UNIPARC:UPI000173B92
C;Comment: Prolines at the carboxyl-terminal position of the tripeptide repeating unit (G-X-Y)
C;Comment: The type III collagen molecule is a trimer of identical chains linked to each
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
C;Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyproli
F;1-14/Product: collagen alpha 1(III) chain #status experimental <CAB>
F;15-1040/Region: amino-terminal nonhelical telopeptide
F;15-1040/Region: helical
F;589-589/Region: cell attachment (R-G-D) motif
F;752-754/Region: cell attachment (R-G-D) motif
F;875-877/Region: cell attachment (R-G-D) motif
F;878-880/Region: cell attachment (R-G-D) motif
F;935-937/Region: cell attachment (R-G-D) motif
F;1041-1049/Region: carboxyl-terminal nonhelical telopeptide
F;107,119,938,950/Modified site: allysine (Lys) #status predicted #status experimental
F;95,107,119,938,950/Modified site: 5-hydroxylysine (Lys) #status experimental
F;107,950/Modified site: carbohydrate (Lys) (covalent) #status predicted
F;1040,1041/Binding site: carbohydrate (Lys) #status experimental
F;1040,1041/Disulfide bonds: interchain #status predicted

Query Match   6.3%; Score 154.5; DB 1; Length 1049;
Best Local Similarity   26.5%;
Matches 60; Conservative   9; Mismatches 74; Indels 83; Gaps   8;

Qy 171 PRGGAVPRKPVSEMPMERDRGA----------------------AHSLEPGKEN 202
         |:| | |:| : | || |||:| |||
Db 688 PAGGSGPAGPPGPQGVKGERGSPGGPGPAAGFPGPGGRGPGPGPPGSNGNPGGP 747

Qy 203 LPGDPTSNAT-------------SRGAEGPLPPPSMPAVAGAAGGLLALLLLGVAGA 245
         |||| |:| | |:|| | || | | | :|
Db 748 PPGPGPGSNGAPGSPGISGPKGDSGPPGERGAPGPGPGPPGAPGPLGIAG----LTGARGL 802

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Qy    246  GGAMCWRRRRAKP------SESRHPGP------GSFGRGGSLGLGGGGGMGPREAEPGE  292
                        :        |||                    :        ||
Db    803  AGPPGMPGARGSPGPQGIKGENGKPGPSGQNGERGPPGPQGLPGLAGTAGEPGRDGNPGS  862

Qy    293  LGIALRGG---------GAADPPFCPHYEKVSGDYGHPVVIVQDGPP  330
                |:      |    |||                |||
Db    863  DGLPGRDGAPGAKGDRGENGSPGAP------GAPGHP-----GPP  896
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